

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 15, 2003, 13:28:23 ; Search time 1435.75 seconds

(without alignments)
10479.665 Million cell updates/sec

Title: US-09-852-261-1

Perfect score: 517

Sequence: 1 ggaacggagagcgtctgcg.....tgaatcacacaagtaaacat 517

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Gapop 10.0 , Gapept 1.0

Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:*

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5: gb_ov:*

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23: em_pat:*

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26: em_ro:*

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31: em_htg_inv:*

32: em_htg_other:*

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 517 | 100.0 | 517 | 6 | AX147742 Sequence |
| 2 | 517 | 100.0 | 517 | 6 | AX300779 Sequence |
| 3 | 467.4 | 90.4 | 523 | 6 | AX147746 Sequence |
| 4 | 467.4 | 90.4 | 523 | 6 | AX300783 Sequence |
| 5 | 377.2 | 73.0 | 471 | 6 | AX147754 Sequence |
| 6 | 377.2 | 73.0 | 471 | 6 | AX300791 Sequence |
| 7 | 355.4 | 68.7 | 444 | 6 | HSU40870 Human alter |
| 8 | 344.2 | 66.6 | 616 | 6 | HSIGF1A |
| 9 | 344.2 | 66.6 | 7260 | 6 | AX375028 Sequence |
| 10 | 344.2 | 66.6 | 7260 | 6 | AX411095 Sequence |
| 11 | 344.2 | 66.6 | 7260 | 6 | AX57025 Human IGF-I |
| 12 | 342.6 | 66.3 | 666 | 6 | A29119 H.sapiens I |
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| 18 | 330 | 63.8 | 798 | 10 | RNIGF12 |
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| 42 | 258.4 | 50.0 | 317 | 6 | AX300787 |
| 43 | 258.4 | 50.0 | 462 | 6 | AX481428 |
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| 45 | 254.2 | 49.2 | 521 | 10 | RNIGFI |

ALIGNMENTS

RESULT 1

AX147742

LOCUS AX147742

DEFINITION Sequence 1 from patent WO0136483.

ACCESSION AX147742

VERSION AX147742.1 GI:14346787

KEYWORDS

SOURCE

ORGANISM

human.

Human sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE

1 (bases 1 to 517)

Goldspink,G.R. and Johnson,I.R.

Use of the insulin-like-growth factor i isoform mgf for the

titlle

treatment of neurological disorders

Pred. No. is the number of results predicted by chance to have a

JOURNAL Patent: WO 0136483-A 1 25-MAY-2001;
University College London (GB)
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BASE COUNT 150 a 130 c 139 g 98 t
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Best Local Similarity 100.0%; Pred. No. 5e-155;
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DB 481 GATGGCATTTCCCAATGAATATACACAAGTAACAT 517
RESULT 2
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LOCUS AX300779
DEFINITION Sequence 1 from Patent WO0185781.
ACCESSION AX300779
VERSION AX300779.1 GI:17382060
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Goldspink, G.D. and Terenghi, G.B.
AUTHORS Repair of nerve damage
TITLE Patent: WO 0185781-A 1 15-NOV-2001;
JOURNAL

University College London (GB) ; East Grinstead Medical Research
Trust (GB)
FEATURES Location/Qualifiers
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BASE COUNT 150 a 130 c 139 g 98 t
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Best Local Similarity 100.0%; Pred. No. 5e-155;
Matches 517; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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AX147746 523 bp DNA linear PAT 08-JUN-2001
LOCUS AX147746
DEFINITION Sequence 5 from Patent WO0136483.
ACCESSION AX147746
VERSION AX147746.1 GI:14346791
KEYWORDS
SOURCE rabbit.
ORGANISM Oryctolagus cuniculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
REFERENCE
1 (bases 1 to 523)
AUTHORS Goldspink, G.R. and Johnson, I.R.
TITLE Use of the insulin-like-growth factor 1 isoform mgf for the
treatment of neurological disorders

JOURNAL Patent: WO 0136483-A 5 25-MAY-2001;
University College London (GB)
FEATURES Location/Qualifiers
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BASE COUNT 154 a 129 c 142 g 98 t
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Query Match 90.4%; Score 467.4; DB 6; Length 523;
Best Local Similarity 96.2%; Pred. No. 4.8e-139;
Matches 501; Conservative 0; Mismatches 16; Indels 4; Gaps 2;

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DB 481 CAAGATGSCATTTCCCCCAATGAATACACAAGTAACAT 521

RESULT 4
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LOCUS AX300783
DEFINITION Sequence 5 from Patent WO0185781.
ACCESSION AX300783
VERSION AX300783.1 GI:17382064
KEYWORDS
SOURCE
ORGANISM Oryctolagus cuniculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

REFERENCE
AUTHORS Goldspink,G.D. and Terenghi,G.B.
TITLE Repair of nerve damage
JOURNAL Patent: WO 0185781-A 5 15-NOV-2001;

University College London (GB) ; East Grinstead Medical Research
Trust (GB)
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BASE COUNT 154 a 129 c 142 g 98 t
ORIGIN

Query Match 90.4%; Score 467.4; DB 6; Length 523;
Best Local Similarity 96.2%; Pred. No. 4.8e-139;
Matches 501; Conservative 0; Mismatches 16; Indels 4; Gaps 2;

QY 1 GGACCGAGAGCGCTCTGCGGGGCTGAGCTGGTGGATGCTTCACTTGTGTGGAGAC 60
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RESULT 5
AX147754 471 bp DNA linear PAT 08-JUN-2001
LOCUS AX147754
DEFINITION Sequence 13 from Patent WO0136483.
ACCESSION AX147754
VERSION AX147754.1 GI:14348552
KEYWORDS
SOURCE
ORGANISM Oryctolagus cuniculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

REFERENCE
AUTHORS Goldspink,G.R. and Johnson,I.R.
TITLE Use of the insulin-like-growth factor I isoform mgf for the
treatment of neurological disorders

| JOURNAL | | Patent: WO 0136483-A 13 25-MAY-2001; | |
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| Query Match | | 73.0%; Score 377.2; DB 6; Length 471; | |
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| Dd | 256 | ---AAGGAATACATTTGAGAAACACAAAGTAGAGGAGTGCAGAAACAAGACTACAG | 311 |
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| Oy | 420 | TGCACAGTACCTGTAAACATTTGGAAATCCGGCCAAAATAATAGTTGATGCATTTCAA | 479 |
| Dd | 372 | TGCACAGTACCTGTAAACATTTGGAAATCCGGCCAAAATAATAGTTGATGCATTTCAA | 431 |
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| Dd | 432 | AGATGGCATTTCCCCCAATGAATACACAGTAATACAT | 469 |
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| DEFINITION | Sequence 13 from Patent WO0185781. | DNA | linear |
| ACCESSION | AX300791 | | |
| VERSION | AX300791.1 | GI:17382072 | |
| KEYWORDS | | | |
| SOURCE | Rabbit. | | |
| ORGANISM | Oryctolagus cuniculus | | |
| REFERENCE | 1 | Goldspink, G.D. and Terenighi, G.B. | |
| AUTHORS | | Repair of nerve damage | |
| TITLE | | Patent: WO 0185781-A 13 15-NOV-2001; | |
| JOURNAL | | | |

University College London (Gb) ; East Grinstead Medical Research Trust (Gb)

FEATURES
 Source Location/Qualifiers
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BASE COUNT 132 a 118 c 131 g 90 t

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Query Match 73.0%; Score 377.2; DB 6; Length 471;
 Best Local Similarity 87.8%; Pred. No. 5.3e-110;
 Matches 455; Conservative 0; Mismatches 13; Indels 50; Gaps 2;

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 DB 432 AGATGGCATTTCCCAATGAATGAATACAGATTAACAT 469

RESULT 7
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 LOCUS HSU40870
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 (IGF-I) mRNA, partial cds.
 ACCESSION U40870
 VERSION U40870.1 GI:1100902
 KEYWORDS Homo sapiens.
 ORGANISM Homo sapiens.
 SOURCE
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 444)
 AUTHORS Chew S.L., Lavender P., Clark A.J. and Ross R.J.
 TITLE An alternatively spliced human insulin-like growth factor-I

transcript with hepatic tissue expression that diverts away from the mitogenic IRE1 peptide
 JOURNAL Endocrinology 136 (5), 1939-1944 (1995)
 MEDLINE 95237119
 PUBMED 7720641
 REFERENCE 2 (bases 1 to 444)
 AUTHORS Chew, S.L.
 TITLE Direct Submission
 JOURNAL Submitted (20-NOV-1995) Shern L. Chew, Endocrinology, St Bartholomew's Hospital Medical College, West Smithfield, London, EC1A 7BE, UK

FEATURES

source Location/Qualifiers
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 /db_xref="taxon:9606"
 /clone="pc4"
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BASE COUNT 107 a 125 c 125 g 87 t
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 Best Local Similarity 99.7%; Pred. No. 5,6e-103; Indels 0; Gaps 0;
 Matches 356; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 DB 88 GGACCGGAGACGCTGCGGGGCTGAGCTGTGATGCTCTTCAGTTCGTGTGTGAGAC 147
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 QY 61 AGGGGCTTTATTATTCACACAGCCCAAGGGTATGCTCTCAGCAGTCCGAGGGCGCTAG 120
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 DB 148 AGGGGCTTTATTATTCACACAGCCCAAGGGTATGCTCTCAGCAGTCCGAGGGCGCTAG 207
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QY 301 AGGAAGAGAGTACATTGAGACACAGTAGAGGAGTGCAGGAACAAGACTA 357
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RESULT 8
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 X56773.1 GI:32989
 IGF-1 gene.
 Homo sapiens.
 Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 AUTHORS Sandberg-Nordqvist, A.C., Stahlbom, P.A., Lake, M. and Sara, V.R.
 TITLE Characterization of two cDNAs encoding insulin-like growth factor 1 (IGF-1) in the human fetal brain

JOURNAL Brain Res. Mol. Brain Res. 12 (1-3), 275-277 (1992)
 MEDLINE 92186627
 PUBMED 1372070
 2 (bases 1 to 616)
 Sandberg-Nordqvist, A.C.
 REFERENCE
 AUTHORS Sandberg-Nordqvist, A.C.
 TITLE Direct Submission
 JOURNAL Submitted (19-NOV-1990) A.C. Sandberg-Nordqvist, KAROLINSKA INST'S DEPT OF PATHOLOGY, KAROLINSKA HOSPITAL, BOX 605 00, S-104 01 SNOCKHOLM, SWEDEN

REFERENCE
 AUTHORS Sandberg-Nordqvist, A.C., Stahlbom, P.A., Reinecke, M., Collins, V.P., von Holst, H. and Sara, V.
 TITLE Characterization of Insulin-like growth factor 1 in human primary brain tumors
 JOURNAL Cancer Res. 53 (11), 2475-2478 (1993)
 MEDLINE 93265440
 PUBMED 8495408

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 Best Local Similarity 87.3%; Pred. No. 2.4e-99; Indels 53; Gaps 5;
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| Dd | 205 | AAGGGCTTTTATTTTCAACAAGCCCAAGGGTATGCTCCAGAGTGGAGGGCGCTTAG | 264 |
| QY | 121 | ACAGGCATGCTGGATGATGATGCTGCTTCGAGAGCTGTGATCTAAGAGAGCTGAGATGTAT | 180 |
| Dd | 265 | ACAGGCATGCTGGATGATGATGCTGCTTCGAGAGCTGTGATCTAAGAGAGCTGAGATGTAT | 324 |
| QY | 181 | TGCGACACCCCTCAAGCCCGCAATGCATGCTGCTGTCGAGCCAGCGCCACACCGAC | 240 |
| Dd | 325 | TGCGACACCCCTCAAGCCCGCAATGCATGCTGCTGTCGAGCCAGCGCCACACCGAC | 384 |
| QY | 241 | ATGCCCAAGACCCAGCAAGTATCAGCCCCCATCTACCAACAAGAACAGAGTCTGAGAGA | 300 |
| Dd | 385 | ATGCCCAAGACCCAG----- | 399 |
| QY | 301 | AAGAAAGGAAGTACTTTTGAAGAACACAATATAGAGGATGTCGAGAAACAAGAACTACAG | 360 |
| Dd | 400 | ---AAGGAAGTACTTTTGAAGAAACGCAAGTATAGGGATGTCGAGAAACAAGAACTACAG | 455 |
| QY | 361 | GATGTA-GAAGACCCCTTCTGAGAGTAGAAGAAGAGACGACACCGCAGGACCTTTGCTC | 419 |
| Dd | 456 | GATGTAAGGAAGACCTCTCTGAGAGTAAAGATGATGATGCAACCGCAGGATCTTTGCTC | 515 |
| QY | 420 | TGCAC-AGTTACCTG-TAACATTGGATATCCGGCCAAAAAATTAAGTTGATACATTTTC | 477 |
| Dd | 516 | TGCAGAGTTACTGTTTAACTTTGGAAACACTTACCCAAAAAATTAAGTTGATACATTTTA | 575 |
| QY | 478 | AAAGAT-GGCATTTCCCCCAATGAAATATACAAAGTAACAT | 517 |
| Dd | 576 | AAAGATGGCGCTTCCCCCAATGAAATATACAAAGTAACAT | 616 |

| RESULT 9 | AX375028 | 7260 bp | DNA | linear | PAT 01-MAR-2002 |
|---------------------------|--|---|-----|--------|-----------------|
| LOCUS | AX375028 | | | | |
| DEFINITION | Sequence 31 from Patent WO0210436. | | | | |
| ACCESSION | AX375028 | | | | |
| VERSION | AX375028.1 | | | | |
| KEYWORDS | GI:19169860 | | | | |
| SOURCE | human. | | | | |
| ORGANISM | Homo sapiens | | | | |
| | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | |
| | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | | | |
| REFERENCE | 1 | | | | |
| AUTHORS | Baak, J. and Mutter, G.L. | | | | |
| TITLE | Prognostic classification of breast cancer | | | | |
| JOURNAL | Patent: WO 0210436-A 31 07-FEB-2002; THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US) ; Baak, Jan (US) | | | | |
| FEATURES | Location/Qualifiers | | | | |
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| Query Match | 66.6%; Score 344.2; DB 6; Length 7260; | | | | |
| Best Local Similarity | 87.3%; Pred. No. 3,46-99; | | | | |
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| DB | 311 | GGACCGGAGACGCTCGCGGGCTGAGCTGGTGGATCTCTTCAGTTCGTGTGGAGAC | 370 | | |
| OY | 61 | AGGGGCTTTATTTCAACAGGCCACAGGATGATGGCTCCAGCAGTCGAGGAGCGCTCAG | 120 | | |
| | | | | | |
| DB | 371 | AGGGGCTTTATTTCAACAGGCCACAGGATGATGGCTCCAGCAGTCGAGGAGCGCTCAG | 430 | | |
| OY | 121 | ACAGCATCGTGGATGATGAGTGGTGGCTTCGGAGCTGTATCTTAAGAGAGCTGGAGATGAT | 180 | | |
| | | | | | |
| DB | 431 | ACAGCATCGTGGATGATGAGTGGTGGCTTCGGAGCTGTATCTTAAGAGAGCTGGAGATGAT | 490 | | |

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| QY | 181 | TGGCACCCTCCAAAGCTGCGCAAGTCAAGCTGCTCTCCGTGCGCAGGCCACCAACGAC | 240 |
| Db | 491 | TGCGCACCTCCAAAGCTGCGCAAGTCAAGCTGCTCTCCGTGCGCAGGCCACCAACGAC | 550 |
| QY | 241 | ATGCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACAGCAACTCACAAGA | 300 |
| Db | 551 | ATGCCCAAGACCCAG----- | 565 |
| QY | 301 | AGCAAGAAGATACATTGTAAGAACACAGTAGAGGAGGTGACAGAAACAAGACTACAG | 360 |
| Db | 566 | ---AAGAGTACATTGTAAGAAGCAGAGTAGAGGAGGTGACAGAAACAAGACTACAG | 621 |
| QY | 361 | GATGTA-GAAGACCCCTTGTAGAGAGTGAAGAAGACACAGCCACCGCAGACCCCTTCTC | 419 |
| Db | 622 | GATGTAGGAAGACCCCTCTGTAGAGAGTGAAGGTATGACATGCCACCGCAGACTCTTCTC | 681 |
| QY | 420 | TGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCCAAAAATAATAGTTGATCATCTTC | 477 |
| Db | 682 | TGCACGAGTTCACCTGTAAACATTGGAACACACTCCAAAAAATAATAGTTGATCATCTTAA | 741 |
| QY | 478 | AAAGAT-GGCATTTCCGCCAATGGAATACACAACTAAACAT | 517 |
| Db | 742 | AAAGATGGCGCTTTCCGCCAATGGAATACACAACTAAACAT | 782 |

| RESULT 10 | AX411095 | 7260 bp | DNA | linear | PAT 14-JUN-2002 |
|-----------------------|--|--------------------------------------|-----|--------|-----------------|
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| DEFINITION | AX411095 | | | | |
| ACCESSION | AX411095 | | | | |
| VERSION | AX411095.1 | GI:21443800 | | | |
| KEYWORDS | | | | | |
| SOURCE | human. | | | | |
| ORGANISM | Homo sapiens | | | | |
| | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | |
| | Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. | | | | |
| REFERENCE | 1 | | | | |
| AUTHORS | Alvares, C., Horne, D., Pers- da -Silva, S. and Vockley, J.G. | | | | |
| TITLE | Gene expression profiles in liver cancer | | | | |
| JOURNAL | Patent: WO 0229103-A 3742 11-APR-2002; | | | | |
| | GENE LOGIC INC (US) | | | | |
| FEATURES | Location/Qualifiers | | | | |
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| | /db_xref="taxon:9606 | | | | |
| | /note="EMBL/GenBank Accession No. X57025" | | | | |
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| Best Local Similarity | 87.3%; Pred. No. 3.4e-99; | | | | |
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| Db | 431 ACAGGATCTGTGATGAGTGGCTGCTTCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490 | | | | |
| QY | 181 TGGCAGCCCTCAAGCCTGCCAAGTCAAGTCTGTGTCGTTGCCAAGCCACACCGAC 240 | | | | |
| Db | 491 TGGCAGCCCTCAAGCCTGCCAAGTCAAGTCTGTGTCGTTGCCAAGCCACACCGAC 550 | | | | |
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| QY | 420 | IGGAC-AGTACCG-7AAACATTGGAAATCCGCCCAAAATAAGTTGATCCATTC | 477 |
|-----------------------|--|--|-----------------|
| Db | 527 | IGGACAGATTACCTGTTAACTTTGGACACCTTACCAAAATAAGTTGATTAACATTTA | 586 |
| QY | 478 | AAAGAT-GGCATTTCCCCCAATGAATAATCAAGATAAACAAT | 517 |
| Db | 587 | AAAGATGGCGGTTCCCCCAATGAATAATCAAGATAAACAAT | 627 |
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| DEFINITION | HUMGFII | 728 bp | RNA |
| VERSION | M29644 | | linear |
| KEYWORDS | M29644.1 GI:183119 | | PRI 08-NOV-1994 |
| SOURCE | Human (adult) liver, cDNA to mRNA. | | |
| ORGANISM | Homo sapiens | | |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| AUTHORS | Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo. | | |
| TITLE | Rall, L.B., Scott, J., and Bell, G.I. | | |
| JOURNAL | Human insulin-like growth factor I and II messenger RNA: isolation | | |
| MEDLINE | of complementary DNA and analysis of expression | | |
| PUBMED | Meth. Enzymol. 146, 239-248 (1987) | | |
| FEATURES | 88065102 | | |
| source | 3683205 | | |
| gene | Location/Qualifiers | | |
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| | /product="insulin-like growth factor I" | | |
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| Best Local Similarity | 87.1% Pred. No. 8e-99; | | |
| Matches | 454; Conservative 0; Mismatches 14; Indels 53; Gaps 5; | | |
| QY | 1 | GGACCGAGAGCGCTCTGCGGCGAGCTGATGCTGATCTTCACTTCTGCTGTGTGGAGAC | 60 |
| Db | 156 | GGACCGAGAGCGCTCTGCGGCGAGCTGATGCTGATCTTCACTTCTGCTGTGTGGAGAC | 215 |
| QY | 61 | AGGCGCTTTATTTTACACAGCCACAGGATATGCTCCAGACATCGGAGAGCGGCTGAC | 120 |
| Db | 216 | AGGCGCTTTATTTTACACAGCCACAGGATATGCTCCAGACATCGGAGAGCGGCTGAC | 275 |
| QY | 121 | ACAGGATCGTGATGCTGCTTCGCGAGCTGATCTTAAGSAGGCTGAGATGAT | 180 |
| Db | 276 | ACAGGATCGTGAGAGATGCTGCTTCGCGAGCTGATCTTAAGSAGGCTGAGATGAT | 335 |
| QY | 181 | TGGGACCCCTCAACCTCGCCAGACAGTGCCTGTGCCGAGCCAGGACACACGAC | 240 |
| Db | 336 | TGGGACCCCTCAACCTCGCCAGACAGTGCCTGTGCCGAGCCAGGACACACGAC | 395 |

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|----|-----|---|-----|
| QY | 241 | ATGCCCAAGACCCGAGAGTATCAGCCCCCATCTCCCAACAGAGACGAAAGTCTCAAGA | 300 |
| | | | |
| Db | 396 | ATGCCCAAGACCCAG----- | 410 |
| QY | 301 | AGGAAGAAGTACATTTGAGAACACAGTAGAGGAGTGCAGAGAAACAAGAAGTACAG | 360 |
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| QY | 361 | GATGTA-GAAGACCTTCTGAGAGTAGAAGAGACAGGCCAGCGAGGACCTTTGCTC | 419 |
| | | | |
| Db | 467 | GATGTAGAAACCTCTCTGAGAGTAGAGGTACATGCCACCGCAGATCTTTGCTC | 526 |
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| | | | |
| Db | 527 | TGCAGGATTAACCTGTTAAACTTTGGAAACACCTCCAAAATAAATAGTTGATCAATTTA | 586 |
| QY | 478 | AAAGAT-GGCATTTCCCCCAATGGAATTCACACAGTAATACAT | 517 |
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| Db | 587 | AAAGATGGCGCTTTCGCCCAATGGAATTCACACAGTAATACAT | 627 |

RESULT 15

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| LOCUS | HUMIGF | 1076 bp | mRNA | linear | PRI 08-NOV-1994 |
| DEFINITION | Human insulin-like growth factor mRNA, complete cds. | | | | |
| ACCESSION | M27544 | | | | |
| VERSION | M27544.1 | GI:184829 | | | |
| KEYWORDS | insulin-like growth factor. | | | | |
| ORGANISM | Human liver, CDNA to mRNA, clones 1anbda-TG[03_04_05]. | | | | |
| SOURCE | Human sapiens | | | | |

REFERENCE

AUTHORS Le Bouc, Y., Dreyer, D., Jaeger, F., Binoux, M. and Schneider-Maeygeest, P.

TITLE Complete characterization of the human IGF-I nucleotide sequence

JOURNAL
ISOLATED FROM A NEWLY CONSTRUCTED ADULT LIVER cDNA LIBRARY
FEBS Lett. 196 (1), 108-112 (1986)

MEDLINE 86108910
PUBMED 2935423

| FEATURES | Location/Qualifiers |
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293.502
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| Weight | | | | |
| Volume | | | | |
| Temperature | | | | |
| Pressure | | | | |
| Humidity | | | | |
| Time | | | | |
| Date | | | | |
| Location | | | | |
| Operator | | | | |
| Instrument | | | | |
| Method | | | | |
| Procedure | | | | |
| Notes | | | | |
| Signature | | | | |
| Initials | | | | |
| Stamp | | | | |
| Label | | | | |
| Barcode | | | | |
| Serial | | | | |
| Lot | | | | |
| Batch | | | | |
| Run | | | | |
| Sample | | | | |
| Test | | | | |
| Result | | | | |
| Conclusion | | | | |
| Recommendation | | | | |
| Comments | | | | |
| Remarks | | | | |
| Observations | | | | |
| Findings | | | | |
| Analysis | | | | |
| Interpretation | | | | |
| Summary | | | | |
| Conclusion | | | | |
| Recommendation | | | | |
| Comments | | | | |
| Remarks | | | | |
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| Findings | | | | |
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| Interpretation | | | | |
| Summary | | | | |
| Conclusion | | | | |
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| Interpretation | | | | |
| Summary | | | | |
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| Recommendation | | | | |
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| Recommendation | | | | |
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| Remarks | | | | |
| Observations | | | | |
| Findings | | | | |
| Analysis | | | | |
| Interpretation | | | | |
| Summary | | | | |
| Conclusion | | | | |
| Recommendation | | | | |
| Comments | | | | |
| Remarks | | | | |
| Observations | | | | |
| Findings | | | | |

ORIGIN Chromosome /p13-p12.

| | | | | |
|-------------|-------|-------------|------|-------------|
| Query Match | 66.3% | Score 342.6 | DB 9 | Length 10/6 |
|-------------|-------|-------------|------|-------------|

Best Local Similarity 87.1%; Pred. No. 8.5e-99;
Matches 454; Conservative 0; Mismatches 14; Indels 53; Gaps 5;

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      293 GGACCGGAGACGCTGCGGGGCTGAGCTGGATGCTCTTCAGTTGCTGTGAGAC 352
      |||
QY      61 AGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCATCGGAGGGCGCTCAG 120
      |||
      353 AGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCATCGGAGGGCGCTCAG 412
      |||
QY      121 ACAGCATCGTGGATGAGTGTGCTTCCGAGCTGTGATCTAAGAGAGCTGAGATGTAT 180
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      413 ACAGCATCGTGGATGAGTGTGCTTCCGAGCTGTGATCTAAGAGAGCTGAGATGTAT 472
      |||
QY      181 TGGCGACCCCTCAACCTGCGCAAGTCACTGCTGTGCTGCGCCAGCGCCACACGAC 240
      |||
      473 TGGCGACCCCTCAACCTGCGCAAGTCACTGCTGTGCTGCGCCAGCGCCACACGAC 532
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QY      241 ATGCCCAAGACCCAGAGATATCAGCCCCATCTACCAACAAGAACGAGTCTCAGAGA 300
      |||
      533 ATGCCCAAGACCCAG----- 547
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QY      301 AGGAAGGAGTACTTTTGAAGACACAGTAGAGGGAGTGCAGGAACAAGAATCTACAG 360
      |||
      548 ----AAGGAAGTACTTTTGAAGAACGCAAGTAGAGGGAGTGCAGGAACAAGAATCTACAG 603
      |||
QY      361 GATGTA-GAAGACCTTCTGAGAGAGTGAAGAAGAGAGCCACCGCAGACCTTTGCTC 419
      |||
      604 GATGTAAGAGAGACCTCTCTGAGAGAGTGAAGAAGTGAATGATGCCACCGCAGATCTTTGCTC 663
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QY      420 TGCAC-AGTTACCTG-TAAGATTGGAATACCGGCCAAAAAATAAGTTGATCAATTTG 477
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      664 TGCACAGATTACCTGTTAAGTTGGAACACCTACCAAAAAAATAAGTTGATCAATTTG 723
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QY      478 AAAGAT-GGCATTTCCCAATGAATACACAGTAACAT 517
      |||
      724 AAAGATGGCGCTTTCCCAATGAATACACAGTAACAT 764
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Search completed: June 15, 2003, 17:22:06
Job time : 1439.75 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 15, 2003, 09:07:57 ; Search time 156.935 Seconds
(without alignments)
7423.602 Million cell updates/sec

Title: US-09-852-261-1

Perfect score: 517
Sequence: 1 ggaacggagacgcctcgcg.....tgaatacaccaagtaaacat 517

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------------------|
| 1 | 517 | 100.0 | 517 | 22 | AAD06398 Human IGF-I isoform |
| 2 | 517 | 100.0 | 517 | 24 | AA516877 Human mechano-growth |
| 3 | 467.4 | 90.4 | 523 | 22 | AA516877 Rabbit IGF-I isoform |
| 4 | 467.4 | 90.4 | 523 | 24 | AA516877 Rabbit mechano-growth |
| 5 | 467.4 | 90.4 | 523 | 18 | AA516877 Rabbit mechano-growth |
| 6 | 377.2 | 73.0 | 471 | 22 | AA006405 Rabbit insulin-like |
| 7 | 377.2 | 73.0 | 471 | 24 | AA516884 Rabbit insulin-like |
| 8 | 344.2 | 66.6 | 818 | 8 | AA516884 Sequence encoding |
| 9 | 344.2 | 66.6 | 7260 | 24 | ABK4583 Human CDNA differe |

| | | | | | |
|----|-------|------|------|----|------------------------------|
| 10 | 344.2 | 66.6 | 7260 | 24 | ABN97244 Gene #3742 used to |
| 11 | 344.2 | 66.6 | 7260 | 24 | ABK64812 Human benign prostr |
| 12 | 344.2 | 66.6 | 7260 | 24 | ABK33504 Human endometrial |
| 13 | 344.2 | 66.6 | 7260 | 24 | ABK33561 Gene IGF-I differer |
| 14 | 342.6 | 66.3 | 777 | 18 | AA516894 Human insulin like |
| 15 | 339.4 | 65.6 | 622 | 7 | AA516894 Human prepro-somat |
| 16 | 325.2 | 62.9 | 539 | 22 | AAD06399 Rat IGF-I isoform |
| 17 | 325.2 | 62.9 | 539 | 22 | AAD06399 Rat mechano-growth |
| 18 | 308.6 | 56.7 | 1136 | 8 | AA516878 Sequence encoding |
| 19 | 286.4 | 55.4 | 3599 | 19 | AAV50428 Plasmid pIG0352 10 |
| 20 | 286.4 | 55.4 | 3599 | 19 | AAV504796 Actual sequence of |
| 21 | 286.4 | 55.4 | 3600 | 19 | AAV50427 Plasmid pIG0552 up |
| 22 | 286.4 | 55.4 | 3600 | 19 | AAV504795 Expected sequence |
| 23 | 286.4 | 55.4 | 5707 | 20 | AA516885 Plasmid pIG0335 DN |
| 24 | 286.4 | 55.4 | 6345 | 20 | AA516885 Plasmid pIG0100A D |
| 25 | 285.4 | 55.2 | 612 | 22 | AA516895 Human CDNA encoding |
| 26 | 271.2 | 52.5 | 978 | 14 | AA041804 Sequence encoding |
| 27 | 258.4 | 50.0 | 317 | 24 | AA516882 Human insulin-like |
| 28 | 258.4 | 50.0 | 318 | 22 | AAD06403 Human liver-type I |
| 29 | 258.4 | 50.0 | 462 | 19 | AAV50426 Human IGF-I encodi |
| 30 | 258.4 | 50.0 | 462 | 19 | AAV40794 Human IGF-I coding |
| 31 | 258.4 | 50.0 | 462 | 24 | AB191699 Human polynucleoti |
| 32 | 252.6 | 48.9 | 1052 | 20 | AA527498 Rat liver form of |
| 33 | 247.8 | 47.9 | 487 | 22 | AAD06404 Rat liver-type IGF |
| 34 | 247.8 | 47.9 | 487 | 22 | AA516883 Rat insulin-like g |
| 35 | 210 | 40.6 | 210 | 24 | ABK03146 Native mature IGF- |
| 36 | 208.4 | 40.3 | 237 | 12 | AA013568 Beta-gal/IGF-1 fus |
| 37 | 208.4 | 40.3 | 238 | 12 | AA013569 Beta-gal/IGF-1 fus |
| 38 | 208.4 | 40.3 | 2862 | 19 | AAV52883 Recombinant botull |
| 39 | 204.6 | 39.6 | 4532 | 24 | AAD32015 Bovine alpha lacta |
| 40 | 203.6 | 39.4 | 210 | 24 | AAD32016 Human insulin-like |
| 41 | 202.8 | 39.2 | 240 | 13 | AAQ23303 Synthetic human IG |
| 42 | 202.8 | 37.3 | 230 | 18 | AA516882 Killer toxin leade |
| 43 | 192.6 | 37.3 | 213 | 21 | AAZ44266 Seq ID 1 used in t |
| 44 | 192.6 | 37.3 | 224 | 21 | AAZ44271 Seq ID 7 used in t |
| 45 | 182.6 | 35.3 | 249 | 21 | AA572015 Single nucleotide |

ALIGNMENTS

RESULT 1
ID AAD06398
AAD06398 standard, CDNA, 517 BP.
XX
XX AAD06398:
XX
XX 10-AUG-2001 (first entry)
XX
XX Human IGF-I isoform mechano-growth factor (MGF) CDNA.

DE Human IGF-I isoform mechano-growth factor (MGF) CDNA.
XX
XX Human, IGF-I isoform; Insulin-like Growth Factor-I; MGF;
KW mechano-growth factor; neurological disorder; neurodegenerative disorder;
KW amyotrophic lateral sclerosis; spinal muscular atrophy; muscular atrophy;
KW polyomyelitis; post-polio syndrome; toxin; motoneuron disorder;
KW nerve damage; autosomal muscular dystrophy; diabetic neuropathy;
KW sex-linked muscular dystrophy; peripheral neuropathy;
KW Alzheimer's disease; Parkinson's disease; ss.
XX
XX Homo sapiens.

| OS | XX | Location/Qualifiers |
|----|----|---|
| XX | XX | 1..333 |
| XX | XX | /*tag= a |
| XX | XX | /product= "Mechano-growth factor (MGF)" |
| XX | XX | /note= "This region comprises exons 3-6. The CDS does |
| XX | XX | not include start codon" |
| XX | XX | /partial |

WO200136483-A1.

XX 25-MAY-2001.

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PF 15-NOV-2000; 2000MO-GB04354.
PR 15-NOV-1999; 99GB-0026968.
XX (UNLO ) UNIV COLLEGE LONDON.
PA Goldslink G, Johnson I;
PI WPI: 2001-355620/37.
XX P-PSDB: AA02447.
DR
XX
PT Use of mechano-growth factor, an isoform of insulin-like Growth
PT Factor-I, capable of reducing motoneuron loss, in the manufacture of a
PT medicament for the treatment of neurological disorder -
XX
XX
PS Claim 4: Page 49-50: 66pp; English.
CC The present invention relates to use of mechano-growth factor (MGF),
CC an insulin-like Growth Factor-I (IGF-I) isoform in the manufacture of a
CC medicament for the treatment of neurological disorder. The MGF is capable
CC of reducing motoneuron loss by 20% or greater in response to nerve
CC avulsion, and effects motoneuron rescue, preferably adult motoneuron
CC rescue. The MGF polynucleotide and polypeptide are useful in the
CC manufacture of a medicament for the treatment of a neurological disorder,
CC including a disorder of motoneurons and/or neurodegenerative disorder,
CC e.g., amyotrophic lateral sclerosis, spinal muscular atrophy, progressive
CC spinal muscular atrophy, infantile or juvenile muscular atrophy,
CC poliomyelitis or post-polio syndrome, a disorder caused by exposure to a
CC toxin, motoneuron trauma, a motoneuron lesion or nerve damage, an
CC injury that affects motoneurons, motoneuron loss associated with aging,
CC autosomal or sex-linked muscular dystrophy, diabetic neuropathy,
CC peripheral neuropathies, Alzheimer's disease and Parkinson's disease.
CC The present sequence is human IGF-I isoform MGF cDNA. MGF is a muscle
CC isoform having extracellular (Ec) domain, hence also referred as
CC IGF-I-Ec. The MGF protein comprises amino acid sequences encoded by
CC nucleic acid sequence of IGF-I exons 4, 5 and 6 in the reading frame
CC of MGF.
XX
SQ Sequence 517 BP; 150 A; 130 C; 139 G; 98 T; 0 other;
Query Match 100.0%; Score 517; DB 22; Length 517;
Best Local Similarity 100.0%; Pred. No. 2e-146;
Matches 517; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 GGACCGGAGAGCGCTGCGGGGCTGAGCTGTGATGCTCTTCAGTTGCTGTGGAGAC 60
QY 61 AGGGGCTTTTATTTCAACAAGCCACAGGATGAGCTCCAGCAGCGAGGGCCCTCAG 120
DB 61 AGGGGCTTTTATTTCAACAAGCCACAGGATGAGCTCCAGCAGCGAGGGCCCTCAG 120
QY 121 ACAGGCATCGTGGATGAGTGTCTCCGAGCTGTGATCTAGAGAGCTGGAGATGAT 180
DB 121 ACAGGCATCGTGGATGAGTGTCTCCGAGCTGTGATCTAGAGAGCTGGAGATGAT 180
QY 181 TCGGCAACCCCTCAAGCTGCGCAAGTCACTGCTGTGCTGCGGCGCCAGCAACGAG 240
DB 181 TCGGCAACCCCTCAAGCTGCGCAAGTCACTGCTGTGCTGCGGCGCCAGCAACGAG 240
QY 241 ATGCCCAAGACCCAGAGTATCAGCCCATCTACCAACAAGAACAGCAAGTCTCAGAGA 300
DB 241 ATGCCCAAGACCCAGAGTATCAGCCCATCTACCAACAAGAACAGCAAGTCTCAGAGA 300
QY 301 AGGAAGAGAGTACTTTGAGAGACACAAAGTAGAGAGGCTGAGAAACAGAACTACAG 360
DB 301 AGGAAGAGAGTACTTTGAGAGACACAAAGTAGAGAGGCTGAGAAACAGAACTACAG 360
QY 361 GATGTAGAGAGACCCCTTCTGAGAGAGTGAAGAGAGAGCCACCCAGAGACCCCTTGTCT 420
DB 361 GATGTAGAGAGACCCCTTCTGAGAGAGTGAAGAGAGAGCCACCCAGAGACCCCTTGTCT 420
QY 421 GCACAGTACCTGTAAACATTGGATACCGGCCCAAAATAAGTTGTATCATATTTCAAA 480

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DB 421 GCACAGTACCTGTAAACATTGGATACCGGCCCAAAATAAGTTGTATCATATTTCAAA 480
QY 481 GATGGCATTTCCCAATGAAATACACAAAGTAACAT 517
DB 481 GATGGCATTTCCCAATGAAATACACAAAGTAACAT 517
RESULT 2
AAS16877 standard; cDNA; 517 BP.
XX ID AAS16877;
XX AAS16877;
XX 25-FEB-2002 (first entry)
DT
XX
XX Human mechano-growth factor (MGF) cDNA.
DE
XX Human mechano-growth factor; Insulin-like growth factor I; IGF-I; MGF;
KW neuroprotective; nerve damage; peripheral nervous system; nerve severing;
KW muscle; neurological disorder; motoneuron loss; motoneuron disorder; ss;
KW nerve avulsion.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
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FT /*note= "No start codon"
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FT /*number= 3
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FT /*tag= c
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FT 308..330
FT /*tag= e
FT /*number= 6
XX
XX WO200185781-A2.
XX
XX 15-NOV-2001.
PD
XX
XX 10-MAY-2001; 2001MO-GB02054.
PF
XX
XX 10-MAY-2000; 2000GB-0011278.
PR
XX
XX (UNLO ) UNIV COLLEGE LONDON.
PA (EGRI-) EAST GRINSTEAD MEDICAL RES TRUST.
XX
XX Goldslink G, Terenghl G;
PI WPI: 2002-055585/07.
XX P-PSDB: AA010539.
DR
XX
PT Use of insulin-like growth factor I (IGF-I) isoform known as
PT mechano-growth factor which is encoded by IGF-I exons 4,5,6 and has
PT ability to reduce motoneuron loss in response to nerve avulsion, to
PT treat nerve damage -
XX
XX Claim 11: Fig 5: 65pp; English.
XX
XX The invention relates to the use of an insulin-like growth factor I
XX (IGF-I) isoform, known as mechano-growth factor (MGF), in the manufacture
XX of a medicament for treating nerve damage in the peripheral nervous
XX system, or for treating nerve damage by localising MGF at the site of
XX damage. The nerve damage may include severing of a nerve. The treatment
XX may be combined with another treatment (such as a polypeptide growth

```


XX Oryctolagus cuniculus.
 XX Key Location/Qualifiers
 XX CDS 1..366
 XX FT /*tag= a
 XX FT /product= "IGF-1"
 XX MO9733997-A1.
 XX 18-SEP-1997.
 XX 11-MAR-1997; 97WO-GB00658.
 XX 11-MAR-1996; 96GB-0005124.
 XX (UNLO) ROYAL FREE HOSPITAL SCHOOL MED.
 XX Goldslink G;
 XX WPI; 1997-470877/43.
 XX P-PSDB; AAM23301.
 XX
 XX Use of insulin like growth factor I characterised by presence of Ec
 XX peptide - to treat humans or animals, particularly muscle disorders,
 XX heart conditions or neuromuscular diseases
 XX
 XX Disclosure: Fig 3; 33pp; English.
 XX
 XX A use of insulin like growth factor I (IGF-1) has been developed, and
 XX is characterised by the presence of the Ec peptide, or a functional
 XX equivalent, in the treatment or therapy of a human or animal. The IGF-1
 XX polypeptide can be used to treat muscular disorders, e.g. Duchenne or
 XX Becker muscular dystrophy, autosomal dystrophies and related progressive
 XX skeletal muscle weakness and wasting, muscle atrophy in ageing humans,
 XX spinal cord injury induced muscle atrophy and neuromuscular diseases,
 XX and cardiac disorders, e.g. diseases where promotion of cardiac muscle
 XX protein synthesis is a beneficial treatment, cardiomyopathies and acute
 XX heart failure or insult, specifically myocarditis or myocardial
 XX infarction. It can also be used to promote bone fracture healing and
 XX maintenance of bone in old age. The present sequence encodes rabbit
 XX IGF-1 used in the present specification.
 XX
 XX Sequence 553 BP; 159 A; 142 C; 147 G; 105 T; 0 other;
 XX
 XX Query Match 90.4%; Score 467.4; DB 18; Length 553;
 XX Best Local Similarity 96.2%; Pred. No. 2.1e-131;
 XX Matches 501; Conservative 0; Mismatches 16; Indels 4; Gaps 2;
 XX
 XX 1 GGACCGGAGACGCTCTGGGGGCTGAGCTGTGATGCTCTTCAGTTGCTGTGGAGAC 60
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 XX 31 GGACCGGAGACGCTCTGGGGGCTGAGCTGTGATGCTCTTCAGTTGCTGTGGAGAC 90
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 XX 61 AGGGGCTTTATTTAAACAAGCCACAGGCTATGGCTCCAGAGCTGGAGGGCGGCTAG 120
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 XX 121 ACAGGATCGTGTGATGAGTGTGCTCGGAGCTGTGATGCTGTGAGGAGCTGAGATGTAT 180
 XX |||||||
 XX 151 ACAGGATCGTGTGATGAGTGTGCTCGGAGCTGTGATGCTGTGAGGAGCTGAGATGTAT 210
 XX |||||||
 XX 181 TGGGCAACCCCTCAAGCTGCCAAGTACGTCTGTCTGTCGCGCCAGCGCCACACGAC 240
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 XX 211 TGTGCACCCCTCAAGCGGCAAGGAGCGCCCTCGCTCCGTCGCGCCAGCGCCACCGAC 270
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 XX 271 ATGCCCAAGATCAGAGATATCAGCCCATCTACCAACAACAAGATGAGTCTAGAGG 330
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 XX 298 AGAAGGAAAGAGATGATTTGAAGACCAAGTAGAGGAGTGCAGGAAACAAAGACTA 357
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QY 358 CAGATGTA-GAAGACCCCTCTGAGGAGTGAAGAGACAGGCGCCAGGACCCCTTTG 416
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 Db 391 CAGGATGTGAGAGACCCCTCTGAGGAGTGAAGAGAGAGAGCCAGGACCCCTTTG 450
 QY 417 CTCTGACAGTACCTGTTAAACATGGAATACCGGCCAAAAATAGTTGATCATTT 476
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 Db 451 CTCTGACAGTACCTGTTAAACATGGAATACCGGCCAAAAATAGTTGATCATTT 510
 QY 477 CAAGATGGCATTTCCCCCAATGAATAACACAGTAACAT 517
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 Db 511 CAAGATGGCATTTCCCCCAATGAATAACACAGTAACAT 551
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 RESULT 6
 AAD06405
 ID AAD06405 standard; cDNA; 471 BP.
 XX
 XX AAD06405;
 XX
 XX 10-AUG-2001 (first entry)
 XX DE
 XX Rabbit liver-type IGF-I isoform (L.IGF-I) cDNA.
 XX
 XX Rabbit; IGF-I isoform; Insulin-like Growth Factor-I; MGF;
 XX mechano-growth factor; neurological disorder; neurodegenerative disorder;
 XX amyotrophic lateral sclerosis; spinal muscular atrophy; muscular atrophy;
 XX polymyositis; post-polio syndrome; toxin; motoneurone disorder;
 XX nerve damage; autosomal muscular dystrophy; diabetic neuropathy;
 XX sex-linked muscular dystrophy; peripheral neuropathy;
 XX Alzheimer's disease; Parkinson's disease; liver; L.IGF-I; ss.
 XX
 XX Oryctolagus cuniculus.
 XX
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 XX /transl_except= (pos:25..27, aa:Gln)
 XX /note= "These translation exceptions occur while decoding
 XX the alternative version of the protein (AAE02456).
 XX The CDS comprises exons 3, 4 and 6 and
 XX does not include start codon"
 XX /partial
 XX
 XX W0200136483-A1.
 XX
 XX 25-MAY-2001.
 XX
 XX 15-NOV-2000; 2000WO-GB04354.
 XX
 XX 15-NOV-1999; 99GB-0026968.
 XX
 XX (UNLO) UNIV COLLEGE LONDON.
 XX
 XX Goldslink G; Johnson I;
 XX
 XX WPI; 2001-355626/37.
 XX P-PSDB; AAE02452; AAE02456.
 XX
 XX Use of mechano-growth factor, an isoform of Insulin-like Growth
 XX Factor-I, capable of reducing motoneurone loss, in the manufacture of a
 XX medicament for the treatment of neurological disorder -
 XX
 XX Disclosure: Page 59-60; 66pp; English.
 XX
 XX The present invention relates to use of mechano-growth factor (MGF),
 XX an Insulin-like Growth Factor-I (IGF-I) isoform in the manufacture of a
 XX medicament for the treatment of neurological disorder. The MGF is capable
 XX of reducing motoneurone loss by 20% or greater in response to nerve
 XX avulsion, and effects motoneurone rescue, preferably adult motoneurone
 XX rescue. The MGF polynucleotide and polypeptide are useful in the
 XX manufacture of a medicament for the treatment of a neurological disorder.--

including a disorder of motoneurons and/or neurodegenerative disorder, e.g., amyotrophic lateral sclerosis, spinal muscular atrophy, progressive spinal muscular atrophy, infantile or juvenile muscular atrophy, poliomyelitis or post-polio syndrome, a disorder caused by exposure to a toxin, motoneuron trauma, a motoneuron lesion or nerve damage, an injury that affects motoneurons, motoneuron loss associated with aging, autosomal or sex-linked muscular dystrophy, diabetic neuropathy, peripheral neuropathies, Alzheimer's disease and Parkinson's disease. The present sequence is rabbit liver-type IGF-I isoform (L-IGF-I) cDNA. The L-IGF-I protein comprises amino acid sequences encoded by nucleic acid sequence of IGF-I exons 4 and 6.

Sequence 471 BP; 132 A; 118 C; 131 G; 90 T; 0 other;

| | | | | |
|-------------|--------|--------------|--------|-------------|
| Query Match | 73.08; | Score 377.2; | DB 22; | Length 471; |
|-------------|--------|--------------|--------|-------------|

Best Local Similarity 87.8%; Pred. No. 4.1e-104;

Matches 455; Conservative 0; Mismatches 13; Indels 50; Gaps 2;

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| Db | 1 | GGACCCGGAAGACGCTCTGCGGSGCTAGCTGCTGATGCTCTTTCAGTTCTGTGTGTGAGAC | 60 |
| Oy | 61 | AGGGGCTTTTATTTCAACAGCCCAAGGGATATGAGCTCAGACAGTCGGAGGGGCTTCAG | 120 |
| Db | 61 | AGGGGCTTTTATTTCAACAGCCCAAGGGATATGAGCTCAGACAGTCGGAGGGGCTTCAG | 120 |
| Oy | 121 | ACAGGCACTGTGGATATAGTCTGCTTCCGAGCTGTGATCTTAAGGAGGCTGGAGATGTAT | 180 |
| Db | 121 | ACAGGCACTGTGGATATAGTCTGCTTCCGAGCTGTGATCTTAAGGAGGCTGGAGATGTAT | 180 |
| Oy | 181 | TGAGCACCCCTCAAGGCTGCCAAGTCACCTGCTGTGCCCTGGCCAGGCCACACCGAC | 240 |
| Db | 181 | TGAGCACCCCTCAAGGCGGCAAGGACACCCGCTTCGTCGTCGCCACAGCCACACCGAC | 240 |
| Oy | 241 | ATGCCCAAGACCCAGAGTATCAGCCCCCATCTACCAACAAGAACGAAAGTCTCAGAGA | 300 |
| Db | 241 | ATGCCCAAGACCTCAG----- | 255 |
| Oy | 301 | AGGAAGAAGATCATTTTGAAGACACAAGTATAGAGGGAGTGCAGGAACAAGAACTACAG | 360 |
| Db | 256 | -----AAGGAAGTCACTTTTAAABAACACAAGTATAGAGGGAGTGCAGGAACAAGAACTACAG | 311 |
| Oy | 361 | GATGTA-GAAGACCCCTTCTGAGAGTGAAGAAGACAGGCGACCGCAGACCCCTTGGCTC | 419 |
| Db | 312 | GAGTGTGGAAGACCCCTTCTGAGAGTGAAGAAGACAGGCGCACCGCAGACCCCTTGGCTC | 371 |
| Oy | 420 | TGACAGATTACGCTTAACATGTGAAATCCGGCCAAAATAATTTGATGATACATTTCAA | 479 |
| Db | 372 | TGCACAGTTTACCTGTAAACATGTAATCGGACCCAAAATAATTTGATGATCATTTCAA | 431 |
| Oy | 480 | AGATGGCATTTTCCCCCAATGAATACACAGTAACAT | 517 |
| Db | 432 | AGATGGCATTTTCCCCCAATGAATACACAGTAACAT | 469 |

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RESULT 7
AAS16884
ID AAS16884 standard; cDNA; 471 BP

```

DT 25-FEB-2002 (first entry)

DE Rabbit insulin-like growth factor I liver-type isoform (L.IGF-I) cDNA.

xx Rabbid; mechano-growth factor; insulin-like growth factor I; IGF-I; MGF;
 KW neuroprotective; nerve damage; peripheral nervous system; nerve severing;
 KW muscle; neurological disorder; motoneuron loss; motoneuron disorder; ss;
 KW nerve avulsion; insulin-like growth factor I liver-type isoform, L.IGF-I;
 xx
 05 *Oryzotylagus cuniculus*.

| AA | FH | Key | Location/Qualifiers |
|----|----|-----|---------------------|
|----|----|-----|---------------------|

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FT      CDS
FT      1..318
FT      /tag= a
FT      /product= "Rabbit L. Ich-1"
FT      /partial
FT      /note= "No start codon"
FT      1..75
FT      /tag= b
FT      /number= exon 3
FT      76..258
FT      /tag= c
FT      /number= exon 4
FT      259..315
FT      /tag= d
FT      /number= exon 6

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PN W0200185781-A2

PD 15-NOV-2001.

PF 10-MAY-2001; 2001WO-GB02054.

PR 10-MAY-2000; 2000GB-0011278.

PA (UNLO) UNIV COLLEGE LONDON.

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DR P-PSDB; AAU10564.

| PT | Use of Insulin-11 |
|----|-------------------|
| PT | Prohormone growth |

PT ability to reduce motoneuron loss in response to nerve avulsion, to treat nerve damage

PS Disclosure; Fig 10; 65pp; English.

The invention relates to the use of an insulin-like growth factor I (IGF-I) isoform, known as mechano-growth factor (MGF), in the manufacture of a medicament for treating nerve damage in the peripheral nervous system, or for treating nerve damage by localising MGF at the site of damage. The nerve damage may include severing of a nerve. The treatment may be combined with another treatment (such as a polypeptide growth factor other than MGF) that prevents or diminishes degeneration of the target organ (for example, muscle) which the damaged nerve innervates, whereby the treatment of the muscle with MGF or a polynucleotide encoding MGF prevents or diminishes degeneration. The method is useful for treating neurological disorders, preferably motoneuron disorders. These methods can reduce motoneuron loss by 20% or greater in response to nerve avulsion. This sequence represents cDNA encoding the rabbit insulin-like growth factor I liver-type isoform (L-IGF-I) used in experiments on motoneuron loss.

Sequence 471 BP; 132 A; 118 C; 131 G; 90 T; 0 other;

| Query Match | 73.08; | Score 377.2; | DB 24; | Length 471; |
|-------------|--------|--------------|--------|-------------|
|-------------|--------|--------------|--------|-------------|

Best Local Similarity 87.8%; Pred. No. 4.1e-104;

| | | | | | | | | | |
|---------|------|--------------|----|------------|-----|--------|-----|------|----|
| Matches | 455; | Conservative | 0; | Mismatches | 13; | Indels | 50; | Gaps | 2; |
|---------|------|--------------|----|------------|-----|--------|-----|------|----|

| | | | | |
|----|--|-----|---|-----|
| OY | | 1 | GACCCGAGACGCTTCGCCGGCGCTGAGCTGTGATGCTCTTCACTTGCTGTGTGTGAGAC | 60 |
| | | | | |
| | | | | |
| Db | | 1 | GCACCAGACGCTCTGCCGCTGTAGGCTGGGATGCTTCAATTGCTGTGTGAGAC | 60 |
| OY | | 61 | AGGGGCTTTATTTCACAACAGCCACAGGATATGGCTCCACCAATCGAAGGCGCCTCAG | 120 |
| | | | | |
| | | | | |
| Db | | 61 | AGGGGCTTTATTTCACAACAGCCACAGGATATGGCTCCACCAATCGAAGGCGCCTCAG | 120 |
| OY | | 121 | ACAGGCATCGTGSATAGTGTGCTTCGGAACGTGATCAAAGAAGGCTGGAGATATAT | 180 |
| | | | | |
| | | | | |
| Db | | 121 | ACAGGCATCGTGSATAGTGTGCTTCGGAACGTGATCAAAGAAGGCTGGAGATATAT | 180 |
| OY | | 181 | TGGCACCCCTCAAGCTGCAAGTACAGTGCCTGTGCCCTGGCCACAGCCACACCGAC | 240 |
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|----|-----|---|-----|
| Db | 181 | TGTGCACCCCTCAAGCGCGCAAGGACAGCCGCTCCGTCCGTGCCACCGCACACCGAC | 240 |
| QY | 241 | ATGCCCAACACCCAGAGATATAGGCCCCCATCTACCAACAAGAACGAACTCTCAAGA | 300 |
| Db | 241 | ATGCCCAACACTAG----- | 255 |
| QY | 301 | AGSAAAGAGATACATTGTAAGAACACAAAGTAGAGGAGTGCAGAAACAAAGACTACAG | 360 |
| Db | 256 | ---AAGGAAGTACATTTTAAABAACACAAGTAGAGGAGTGCAGAAACAAAGACTACAG | 311 |
| QY | 361 | GATGTA-GAAGACCCCTTCTGAGAGTGAAGAAAGACAGGCCACCGCAGACCCCTTGCCTC | 419 |
| Db | 312 | GATGTAGSAAAGACCCCTTCTGAGAGTGAAGAAAGACAGGCCACCGCAGACCCCTTGCCTC | 371 |
| QY | 420 | TGCACAGTTAACCTGTAAACATTGGAAATACCGSGCCAAAAAATAAGTTGATACATTCCAA | 479 |
| Db | 372 | TGCACAGTTAACCTGTAAACATTGGAAATACCGSGCCAAAAAATAAGTTGATACATTCCAA | 431 |
| QY | 480 | AGATGGCATTTCCCCCAATGAATAACACAAAGTAAACAT | 517 |
| Db | 432 | AGATGGCATTTCCCCCAATGAATAACACAAAGTAAACAT | 469 |

| | Best Local Similarity | 87.3%; | Pred. No. 5.1e-94; | |
|---------|-----------------------|---|--------------------|----------------------------------|
| Matches | 455; | Conservative | 0; | Mismatches 13; Indels 53; Gaps 5 |
| QY | 1 | GCACCGGAACGCTCTGGGGGCTGAGCTGATGATGCTCTTCAGTTGCTGTGGAGAC | 60 | |
| | | | | |
| Db | 203 | GGACCGGAACGCTCTGGGGGCTGAGCTGATGATGCTCTTCAGTTGCTGTGGAGAC | 262 | |
| | | | | |
| QY | 61 | AGAGGCTTTATTTACACAGGCCACAGGATGAGGCTCCAGAGCTGGAGGGGCTCAG | 120 | |
| | | | | |
| Db | 263 | AGAGGCTTTATTTACACAGGCCACAGGATGAGGCTCCAGAGCTGGAGGGGCTCAG | 322 | |
| | | | | |
| QY | 121 | ACAGGCATCGTGGATGAGTGTCTTCCGAGCTGTATCTAAAGAGGCTGGAGATGAT | 180 | |
| | | | | |
| Db | 323 | ACAGGCATCGTGGATGAGTGTCTTCCGAGCTGTATCTAAAGAGGCTGGAGATGAT | 382 | |
| | | | | |
| QY | 181 | TGCGCACCCCTCAAGCTTGCACATGTGCTGTGCTGGCCACGCGCCACACCGAC | 240 | |
| | | | | |
| Db | 383 | TGCGCACCCCTCAAGCTTGCACATGTGCTGTGCTGGCCACGCGCCACACCGAC | 442 | |
| | | | | |
| QY | 241 | ATGCCCAAGACCAAGATGATCAGGCCCATCTCAACAAAGAAAGAGATCTCAGAG | 300 | |
| | | | | |
| Db | 443 | ATGCCCAAGACCAAGATGATCAGGCCCATCTCAACAAAGAAAGAGATCTCAGAG | 457 | |

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| XX | RESULT 8 |
| XX | AAAT70436 |
| ID | AAAT70436 standard; cDNA; 818 BP. |
| XX | |
| AC | AAAT70436; |
| XX | |
| DT | 05-APR-1991 (first entry) |
| DE | Sequence encoding insulin-like growth factor 1A (IGF-1A). |
| XX | |
| KM | Growth promoter; lactation enhancer; cell proliferation; ss. |
| OS | Homo sapiens. |
| PN | EP229750-A. |
| XX | |
| PD | 22-JUL-1987. |
| XX | |
| PF | 06-JAN-1987; 87EP-0870001. |
| XX | |
| FR | 20-NOV-1986; 86US-0929671. |
| PR | 07-JAN-1986; 86US-0816662. |
| XX | |
| PA | (UNIM) UNIV OF WASHINGTON. |
| XX | |
| PI | Krivt GG, Rotwein PS; |
| XX | |
| DR | WPI; 1987-200203/29. |
| XX | |
| PT | New pre-pro-insulin-like growth factor-1 protein - obid. by |
| PT | recombinant DNA procedures for use as growth promoters for |
| PT | enhancing lactation, for stimulating cell proliferation etc. |
| XX | |
| PS | Example; Fig 5; 59pp; English. |
| XX | |
| CC | A 42 base oligonucleotide corresponding to the DNA sequence encoding |
| CC | amino acids 10 to 23 of mature human IGF-I was synthesized (AAAT70437) |
| CC | The radiolabeled 42 mer was then employed to screen for IGF-I |
| CC | containing DNA sequences in a human liver cDNA library. Insulin- |
| CC | like growth factors-1A and -1B cDNAs were isolated from a human cDNA |
| CC | library by using lambdaagt 11 (AAAT70435, AAAT70436). The human IGF-1 |
| CC | genomic gene was isolated and mapped. It encodes at least two |
| CC | proinsulin-like growth factor-1 proteins. An essentially pure |
| CC | proinsulin-like growth factor-1 protein comprising the sequence |
| CC | of amino acids shown in Figure six is claimed (AAP70277). |
| XX | |
| XX | |
| XX | Sequence 818 BP; 232 A; 186 C; 187 G; 213 T; 0 other; |
| XX | |
| Query Match | 66.6%; Score 344.2; DB 8; Length 818; |

| | | | | |
|----------|--|---|---|----------|
| Db | 458 | ---- | AAGGAAGTACATTGTTAGAGAACGCAAGTAGAGGGAGTGTCAGAGAAACAGAACTACAG | 513 |
| Oy | 361 | GATGTA | -GAAGACCCCTTCTGAGAGTGAAGAAGCAGACGCCACCGCAGACCCCTTGGTC | 419 |
| Db | 514 | GATGTAGGAAGACCCCTCCGAGGAGTGAAGATGACATGCCACCGCAGATCCCTTGGTC | | 573 |
| Oy | 420 | TGTAC | -AGTTACCTG-TAAACATTGGATTACCGGCCAAAAATTAAGTTATCATTC | 477 |
| Db | 574 | TGCACAGATTACCTGTTAACTTTGGAAACACCTACCAAAAAATTAAGTTTATACATTTA | | 633 |
| Oy | 478 | AAAGAT | -GGCAATTCCCCCAATGAATACACAGTAAACAT | 517 |
| Db | 634 | AAAGATGGGCGTTTCCCCCAATGAATACACAAATTAACAT | | 674 |
| RESULT 9 | | | | |
| ABK84583 | | | | |
| ID | ABK84583 | standard; | CDNA; | 7260 BP. |
| XX | ABK84583; | | | |
| AC | | | | |
| XX | | | | |
| DT | 14-AUG-2002 | (first entry) | | |
| XX | | | | |
| DE | Human | CDNA differentially expressed in granulocytic cells #1154. | | |
| XX | Human; | ss; granulocytic cell; DNA chip; bacterial infection; | | |
| KW | Human infection; parasitic infection; protozoal infection; | | | |
| KW | fungus infection; sterile inflammatory disease; psoriasis; | | | |
| KW | rheumatoid arthritis; glomerulonephritis; asthma; thrombosis; | | | |
| KW | cardiac reperfusion injury; renal reperfusion injury; ARDS; | | | |
| KW | adult respiratory distress syndrome; inflammatory bowel disease; | | | |
| KW | Crohn's disease; ulcerative colitis; periodontal disease; | | | |
| KW | granulocyte activation; chronic inflammation; allergy. | | | |
| XX | | | | |
| OS | Homo sapiens. | | | |
| XX | | | | |
| PN | W0200228999-A2. | | | |
| XX | | | | |
| PD | 11-APR-2002. | | | |
| XX | | | | |
| PF | 03-OCT-2001; 2001WO-US30821. | | | |
| XX | | | | |
| PR | 03-OCT-2000; 2000US-237189P. | | | |
| XX | | | | |
| PA | (GENE-) GENE LOGIC INC. | | | |
| XX | | | | |
| DI | Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J; | | | |
| XX | | | | |

DR WPI: 2002-435328/46.

PT Detecting granulocyte activation by detecting differential expression
of genes associated with granulocyte activation, which serves as
diagnostic markers that is useful for monitoring disease states and
drug toxicity

PS Claim 1; SEQ ID NO 1154; 114bp; English.

CC The invention relates to detecting (M1) granulocyte (GC) activation
(GCA), by detecting the level of expression of gene(s) (Gs) identified by
DNA chip analysis as given in the specification, and comparing
the expression level to an expression level in an unactivated
GC, where differential expression of Gs is indicative of GCA.
Also included are modulating (M2) GA by contacting GC with an agent
that alters the expression of at least one gene in GS: (2) screening (M3)
for an agent capable of modulating GCA or an inflammation (especially
chronic) in a tissue, an allergic response in a subject, exposure of a
subject to a pathogen or sterile inflammatory disease using the
gene expression profile; (3) detecting (M4) an inflammation (especially
chronic) in a tissue, an allergic response in a subject, exposure of a
subject to a pathogen or sterile inflammatory disease, by detecting the
level of expression in a sample of the tissue of gene(s) from GS, where
the level of expression of the gene is indicative of inflammation;
(4) treating (M5) an inflammation (especially chronic) or in a tissue,
an allergic response in a subject, exposure of a subject to a pathogen
or sterile inflammatory disease, by contacting a tissue having
inflammation with an agent that modulates the expression of gene(s)
from GS in the tissue. M1 is useful for detecting GCA; M2 is useful for
modulating GA; M3 is useful for screening an agent capable of modulating
GCA preferably in an inflammation in a tissue; M4 is useful for
detecting an inflammation (especially chronic) in a tissue, an allergic
response in a subject, exposure of a subject to a pathogen or sterile
inflammatory disease (e.g., psoriasis, rheumatoid arthritis,
glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal
transplantation, ARDS, adult respiratory distress syndrome,
inflammatory bowel disease, Crohn's disease, ulcerative colitis,
periodontal disease, also bacterial infection, viral infection,
parasitic infection, protozoal infection, fungal infection, and M5 is
useful for treating one of the above conditions. The present
sequence represents a gene differentially expressed in granulocytes.
Note: The sequence data for this patent did not form part
of the printed specification, but was obtained in electronic
format directly from WIPO at
[ftp.wipo.int/pubd/published_pct_sequences](http://wipo.int/pubd/published_pct_sequences).

XX

SO Sequence 7260 BP; 2330 A; 1415 C; 1240 G; 2275 T; 0 other;

Query Match 66.6%; Score 344.2; DB 24; Length 7260;
Best Local Similarity 87.3%; Pred. No. 1,2e+93;
Matches 455; Conservative 0; Mismatches 13; Indels 53; Gaps 5

OY 1 GGACCGGAAGACGCTCGCGGGGCTGAGTGATGATGCTCTTCAGTTCGTGTGGAGAC 60
DB | |||||
OY 311 GGACCGGAAGACGCTCGCGGGGCTGAGTGATGATGCTCTTCAGTTCGTGTGGAGAC 370
DB | |||||
OY 61 AGGGGGTTTATTATTAACAAGGCCCAAGGGATATGGTCACAGACTGGAGGGGCGCTCAG 120
DB | |||||
OY 371 AGGGGCTTTATTATTAACAAGGCCCAAGGGATATGGTCACAGACTGGAGGGGCGCTCAG 430
DB | |||||
OY 121 ACAGGATCGTGATGATGAGTGCTCTTCGGAAGCTGTATCTAAGAGAGCTGGAGATGAT 180
DB | |||||
OY 431 ACAGGATCGTGATGATGAGTGCTCTTCGGAAGCTGTATCTAAGAGAGCTGGAGATGAT 490
DB | |||||
OY 181 TTGGACACCCCTAAACCTGCCAAGTCACACTGGCTCTGTCCGTGCCACAGCCACACCAGAC 240
DB | |||||
OY 491 TTGGACACCCCTAAAGCTGCCAAGTCACACTGGCTCTGTCCGTGCCACAGCCACACCAGAC 550
DB | |||||
OY 241 ATGCCCAAACACCCAGAGATATAGCCCCCACTACCAACAAGAACAAGAGTCTCAGAGA 300
DB | |||||
OY 551 ATGCCCAAACACCCAG----- 565
DB | |||||
OY 301 AGGAAAGAGATGATCATTTTGAAGACACAGATGAGAGGAGTGCACAGAAACAGACTACAG 360

| | | | | |
|-----------------------|---|--|--|--------------|
| Dd | 566 | ---- | AAGGAGGTACATTTTGAAGACCAAGTAGAGGGAGTCGAGAAACAAGAATCAG | 621 |
| Oy | 361 | GATGTA-GAAGACCCTTCTGAGAGTAGAAGAGACAGCCACCGACAGACCTTTCTC | 419 | |
| Dd | 622 | GATGTAGAGAACCCCTCTCTGAGAGTAGAAGTAGACATGCCACCGACAGATCTTGCTC | 681 | |
| Oy | 420 | TGCAC-AGTACTCTG-TAAACATTGGAARACCGGCCAAAAATAAGTTGATCATTTTC | 477 | |
| Dd | 682 | TGCACGAGTTACTGTGTTAAACCTTGGAAACCTCACAAAATAAGTTGATTAACATTTA | 741 | |
| Oy | 478 | AAAGAT-GGCATTCCCCCATGAATACACACAGTAACAT | 517 | |
| Dd | 742 | AAAGATGGCGCTTCCCCCAATGAATACACAGTAACAT | 782 | |
| | | | | |
| RESULT 10 | | | | |
| ABN97244 | | | | |
| ID | ABN97244 | standard; DNA; | 7260 BP. | |
| XX | ABN97244: | | | |
| AC | ABN97244: | | | |
| Dt | 13-AUG-2002 | (first entry) | | |
| XX | | | | |
| De | Gene #3742 | used to diagnose liver cancer. | | |
| KW | Gene: liver cancer; ds: hepatocellular carcinoma; hepatotropic; | | | |
| KW | metastatic liver tumor; cytostatic; expression profile; disease state; | | | |
| KX | disease progression; drug toxicity; drug efficacy; drug metabolism. | | | |
| OS | Homo sapiens. | | | |
| FN | M0200229103-A2. | | | |
| Pd | 11-Apr-2002. | | | |
| XX | 02-OCT-2001; 2001MO-US30589. | | | |
| PR | 02-OCT-2000; 2000US-237054P. | | | |
| PA | (GENE-) GENE LOGIC INC. | | | |
| EI | Horne D, Alvares C, Peres-Da-Silva S, Vockley JG; | | | |
| WP: | 2002-426119/45. | | | |
| PT | Diagnosing and detecting the progression of liver cancer, | | | |
| PT | hepatocellular carcinoma or metastatic liver tumor in a patient, | | | |
| PT | involves detecting the level of expression of two or more genes in a | | | |
| PT | liver tissue sample | | | |
| XX | | | | |
| PS | Claim 1; SEQ ID NO 3742; 298bp; English. | | | |
| XX | The invention relates to a novel method for diagnosing and detecting the | | | |
| CC | progression of liver cancer, hepatocellular carcinoma or metastatic liver | | | |
| CC | tumour in a patient, and differentiating metastatic liver cancer from | | | |
| CC | hepatocellular carcinoma in a patient, involving detecting the level of | | | |
| CC | expression of two or more genes represented in ABN93503-ABN97455 in a | | | |
| CC | tissue sample. The method of the invention has hepatotropic, and | | | |
| CC | cytostatic activity. The method is useful for diagnosing and detecting | | | |
| CC | the progression of liver cancer, hepatocellular carcinoma and metastatic | | | |
| CC | liver carcinoma in a patient. The method is useful for identifying | | | |
| CC | expression profiles which serve as useful diagnostic markers as well as | | | |
| CC | markers that can be used to monitor disease states, disease progression, | | | |
| CC | drug toxicity, drug efficacy and drug metabolism. | | | |
| CC | Note: The sequence data for this patent did not form part of the printed | | | |
| CC | specification, but was obtained in electronic format directly from WIPO | | | |
| CC | at ftp.wipo.int/pub/published_pct_sequences. | | | |
| XX | | | | |
| SQ | Sequence 7260 BP; 2330 A; 1415 C; 1240 G; 2275 T; 0 other; | | | |
| | | | | |
| Query Match | 66.6% | Score 344.2 | DB 24; | Length 7260; |
| Best Local Similarity | 87.3% | Ped No. 1.2e-93; | | |

AC ABR35504;
 XX
 DT 08-MAY-2002 (first entry)
 DE Human endometrial cancer related gene, IGFL
 XX
 XX Human endometrial cancer; differential expression;
 KM Human; ds; gene: endometrial cancer; differential expression;
 KM DNA microarray; protein microarray.
 XX
 OS Homo sapiens.
 PN WO200209573-A2.
 PD 07-FEB-2002.
 XX
 PF 31-JUL-2001: 2001WO-US24104.
 XX
 PR 31-JUL-2000: 2000US-221735P.
 XX
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
 XX
 PI Mutter GL;
 XX
 DR WPI: 2002-179967/23.
 DR P-PSDB: AAU84284.
 XX
 PT Diagnosing endometrial cancer comprises determining expression of
 PT nucleic acid molecules or expression products that are differentially
 PT expressed in normal and malignant endometrium -
 XX
 PS Claim 1: Page 85-89; 233pp; English.
 XX
 CC The invention relates to diagnosing endometrial cancer in a subject
 CC suspected of having endometrial cancer comprising determining the
 CC expression of a set of nucleic acid molecules or expression products in
 CC an endometrial sample suspected of being cancerous, where the set of
 CC nucleic acid molecules comprises at least 2 nucleic acid molecules
 CC selected from 50 fully defined sequences as given in the specification.
 CC The nucleic acids are used as an array of at least 2 of the 50
 CC nucleic acids bound to a solid substrate. Also included is a solid-phase
 CC protein microarray comprising at least 2 antibodies or its antigen
 CC binding fragments, that specifically bind at least 2 different
 CC polypeptides from the 50 fully defined sequences as given in the
 CC specification, fixed to a solid substrate. The methods and arrays are
 CC useful for the diagnosis of endometrial cancer, selecting and monitoring
 CC treatment regimens and identification of lead compounds useful for the
 CC treatment of endometrial cancer. The present sequence is one of 50
 CC genes differentially expressed between cancerous and non-cancerous
 CC samples.
 XX
 SO Sequence 7260 BP; 2330 A; 1415 C; 1240 G; 2275 T; 0 other:
 Query Match 66.6%; Score 344.2; DB 24; Length 7260;
 Best Local Similarity 87.3%; Pred. No. 1.2e-93;
 Matches 455; Conservative 0; Mismatches 13; Indels 53; Gaps 5;
 QY 1 GGACCGAGACGCTGCGGGGTGAGCTGAGATGCTTCACTGCTGTGTGAGAC 60
 DB 311 GGACCGAGACGCTGCGGGGTGAGCTGAGATGCTTCACTGCTGTGTGAGAC 370
 QY 61 AGGCGCTTTTATTCAACAAGCCACAGGGTATGGCTCAGCAGATCGAGGGCGCTCAG 120
 DB 371 AGGCGCTTTTATTCAACAAGCCACAGGGTATGGCTCAGCAGATCGAGGGCGCTCAG 430
 QY 121 ACGAGGATGTGATGATGAGTGTGCTCCGAGCTGTGATCTAAGAGGCTGAGATGAT 180
 DB 431 ACGAGGATGTGATGATGAGTGTGCTCCGAGCTGTGATCTAAGAGGCTGAGATGAT 490
 QY 181 TGGCAACCCCTCAAGCTGCCAAGTCAGCTGCTGTGTGCCAGGCCACACCGAC 240
 DB 491 TGGCAACCCCTCAAGCTGCCAAGTCAGCTGCTGTGTGCCAGGCCACACCGAC 550
 QY 241 ATGCCCAAGACCAAGATATGAGCCCATCTACCAACAAGACGAGTCTCAGAGA 300

DB 551 ATGCCCAAGACCCAG----- 565
 QY 301 AGCAAGCAAGTACATTGTAAGACACACAGTACAGAGGATGCGAGGAACAGACTACAG 360
 DB 566 ---AAGCAAGTACATTGTAAGACACAGTACAGAGGATGCGAGGAACAGACTACAG 621
 QY 361 GATGTA-GAAGACCCCTCTGAGAGTGAAGAGACAGCCACCGCAGACCTTGTCTC 419
 DB 622 GATGTAGGAAGACCCCTCTGAGAGTGAAGAGACAGTGCACCGCAGATCCTTGTCTC 681
 QY 420 TGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAGTTGATACATTTC 477
 DB 682 TGCACAGATTACCTGTTAAACTTTGAAACACCTACAAAAAATAGTTGATACATTTC 741
 QY 478 AAGAT-GGCATTTCCCCCAATGAATACACAGTAACAT 517
 DB 742 AAGATGGGGCTTCCCCCAATGAATACACAGTAACAT 782
 RESULT 13
 ID ABR35561 standard; DNA; 7260 BP.
 AC ABR35561;
 XX
 DT 08-MAY-2002 (first entry)
 DE Gene IGFL differentially expressed in breast cancer tissue.
 XX
 KM Human; diagnosis of breast cancer; endometrial cancer; breast tumour;
 KM MAI; mitotic activity index; cytostatic; gene; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200210436-A2.
 PD 07-FEB-2002.
 XX
 PF 27-JUL-2001: 2001WO-US33642.
 XX
 PR 28-JUL-2000: 2000US-222093P.
 XX
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
 PA (BAK/) BAK J.
 XX
 PI Baak J. Mutter GL;
 XX
 DR WPI: 2002-180084/23.
 DR P-PSDB: AAU84341.
 XX
 PT Diagnosing breast cancer comprises determining expression of nucleic
 PT acid molecules or expression products that are differentially expressed
 PT in normal and malignant tissue -
 XX
 PS Claim 1: Page 74-78; 219pp; English.
 XX
 CC The present invention relates to a method for diagnosing breast cancer
 CC in a subject suspected of having endometrial cancer. The method
 CC comprises determining the expression of a set of human genes or
 CC expression products in an endometrial sample suspected of being
 CC cancerous. The human genes of the invention are differentially
 CC expressed in breast tumours characterised as high or low MAI (mitotic
 CC activity index). These sets of genes can be used to discriminate between
 CC high and low MAI breast tumours. The invention also provides DNA and
 CC protein microarrays for analysing the expression of the human genes and
 CC their protein products. The methods and arrays are useful for the
 CC diagnosis and prognosis of endometrial cancer, selecting and monitoring
 CC treatment regimens, and identification of compounds useful for the
 CC treatment of endometrial cancer. ABR35531-ABR35581 represent the human
 CC genes of the invention that are differentially expressed in breast
 CC cancer tissue.
 XX

SQ Sequence 7260 BP; 2330 A; 1415 C; 1240 G; 2275 T; 0 other;

Query Match 66.6%; Score 344.2; DB 24; Length 7260;
Best Local Similarity 87.3%; Pred. No. 1.2e-93;
Matches 455; Conservative 0; Mismatches 13; Indels 53; Gaps 5;

QY 1 GGACCGGAGAGCGCTCGGGGGCTGAGCTGGTGGATCTCTTCACTGCTGTGTGGAGAC 60
DB 311 GGACCGGAGAGCGCTCGGGGGCTGAGCTGGTGGATCTCTTCACTGCTGTGTGGAGAC 370

QY 61 AGGGGCTTTTATTTCACCAAGCCACAGGGTATGCTCTCCAGAGTCGGAGGCGGCTCAG 120
DB 371 AGGGGCTTTTATTTCACCAAGCCACAGGGTATGCTCTCCAGAGTCGGAGGCGGCTCAG 420

QY 121 ACAGGCACTGATGATGATGCTGCTCCGAGGCTGTGATCTAAGAGAGGCTGGAGATGTAT 180
DB 431 ACAGGCACTGATGATGATGCTGCTCCGAGGCTGTGATCTAAGAGAGGCTGGAGATGTAT 480

QY 181 TGGCCACCCCTCAAGGCTGCCAGAGTCAGTCTGCTCTGCGGCCAGGCGCCACACCGAC 240
DB 491 TGGCCACCCCTCAAGGCTGCCAGAGTCAGTCTGCTCTGCGGCCAGGCGCCACACCGAC 550

QY 241 ATGCCCAAGACCCGAGGATACAGCCCCCATCTACCAACAAGAACAGAGTCTCAGAGA 300
DB 551 ATGCCCAAGACCCGAGGATACAGCCCCCATCTACCAACAAGAACAGAGTCTCAGAGA 565

QY 301 AGGAAGAGAGTACATTGGAAGACACAGTAGAGGAGTGCAGAGAAACAGAACTACAG 360
DB 566 ---AAGGAAGTACATTGGAAGACACAGTAGAGGAGTGCAGAGAAACAGAACTACAG 621

QY 361 GATGTA-GAAGACCCCTCTGAGAGTGAAGAGACAGGCGCCAGGACCTTTGCTC 419
DB 622 GATGTAAGAACCCCTCTGAGAGTGAAGAGTGAAGTGCACCGCGAGATCCTTTGCTC 681

QY 420 TGCAC-AGTTACTG-TAAACATGGAATACCGGCGCAAAAATAGTTATACATTTTC 477
DB 682 TGCACAGATTACCTGTTAACTTTGGAACACCTACCAAAAATAGTTATACATTTTA 741

QY 478 AAGAT-GGCAATTTCCCAATGAATACACAAAGTAACAT 517
DB 742 AAGATGGGCGTTTCCCCCAATGAATACACAAAGTAACAT 782

RESULT 14
AAT84894
ID AAT84894 standard; cDNA; 777 BP.

AC AAT84894;
XX
DT 14-APR-1998 (first entry)
XX
DE Human insulin like growth factor 1 Ea isoform encoding cDNA.
XX
XX Insulin like growth factor 1; IGF-1; Ec peptide; muscle disorder;
KM heart; neuromuscular disease; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 26..496
FT /tag= a
FT /product= "IGF-1 Ea isoform"
XX
XX MO9733997-A1.
XX
XX 18-SEP-1997.
XX
XX 11-MAR-1997; 97WD-GB00658.
XX
XX 11-MAR-1996; 96GB-0005124.
XX
XX (UNLO) ROYAL FREE HOSPITAL SCHOOL MED.

PI Goldslink G;
XX
DR WPI, 1997-470877/43.
DR P-PSDB; AAN60490.
XX
XX
PT Use of insulin like growth factor I characterised by presence of Ec
PT peptide - to treat humans or animals, particularly muscle disorders,
PT heart conditions or neuromuscular diseases
XX
PS Disclosure; Fig 4; 33pp; English.
XX
XX A use of insulin like growth factor I (IGF-1) has been developed, and
CC is characterised by the presence of the Ec peptide, or a functional
CC equivalent, in the treatment or therapy of a human or animal. The IGF-1
CC polypeptide can be used to treat muscular disorders, e.g. Duchenne or
CC Becker muscular dystrophy, autosomal dystrophies and related progressive
CC skeletal muscle weakness and wasting, muscle atrophy in ageing humans,
CC spinal cord injury induced muscle atrophy and neuromuscular diseases,
CC and cardiac disorders, e.g. diseases where promotion of cardiac muscle
CC protein synthesis is a beneficial treatment, cardiomyopathies and acute
CC heart failure or insult, specifically myocarditis or myocardial
CC infarction. It can also be used to promote bone fracture healing and
CC maintenance of bone in old age. The present sequence encodes human
CC IGF-1 Ea isoform used in the present specification.
XX
SQ Sequence 777 BP; 201 A; 193 C; 204 G; 179 T; 0 other;

Query Match 66.3%; Score 342.6; DB 18; Length 777;
Best Local Similarity 87.1%; Pred. No. 1.5e-93;
Matches 454; Conservative 0; Mismatches 14; Indels 53; Gaps 5;

QY 1 GGACCGGAGAGCGCTCGGGGGCTGAGCTGGATGCTCTTCACTGCTGTGTGGAGAC 60
DB 179 GGACCGGAGAGCGCTCGGGGGCTGAGCTGGATGCTCTTCACTGCTGTGTGGAGAC 238

QY 61 AGGGGCTTTTATTTCACCAAGCCACAGGGTATGCTCTCAGAGTGGAGGCGGCTCAG 120
DB 239 AGGGGCTTTTATTTCACCAAGCCACAGGGTATGCTCTCAGAGTGGAGGCGGCTCAG 298

QY 121 ACAGGCACTGATGATGATGCTGCTCCGAGGCTGTGATCTAAGAGAGGCTGGAGATGTAT 180
DB 299 ACAGGCACTGATGATGATGCTGCTCCGAGGCTGTGATCTAAGAGAGGCTGGAGATGTAT 358

QY 181 TGGCCACCCCTCAAGGCTGCCAGAGTCAGTCTGCTCTGCGGCCAGGCGCCACACCGAC 240
DB 359 TGGCCACCCCTCAAGGCTGCCAGAGTCAGTCTGCTCTGCGGCCAGGCGCCACACCGAC 418

QY 241 ATGCCCAAGACCCGAGGATACAGCCCCCATCTACCAACAAGAACAGAGTCTCAGAGA 300
DB 419 ATGCCCAAGACCCGAGGATACAGCCCCCATCTACCAACAAGAACAGAGTCTCAGAGA 433

QY 301 AGGAAGAGAGTACATTGGAAGACACAGTAGAGGAGTGCAGAGAAACAGAACTACAG 360
DB 434 ---AAGGAAGTACATTGGAAGACACAGTAGAGGAGTGCAGAGAAACAGAACTACAG 489

QY 361 GATGTA-GAAGACCCCTCTGAGAGTGAAGAGACAGGCGCCAGGACCTTTGCTC 419
DB 490 GATGTAAGAACCCCTCTGAGAGTGAAGAGTGAAGTGCACCGCGAGATCCTTTGCTC 549

QY 420 TGCAC-AGTTACTG-TAAACATGGAATACCGGCGCAAAAATAGTTATACATTTTC 477
DB 550 TGCACAGATTACCTGTTAACTTTGGAACACCTACCAAAAATAGTTATACATTTTA 609

QY 478 AAGAT-GGCAATTTCCCAATGAATACACAAAGTAACAT 517
DB 610 AAGATGGGCGTTTCCCCCAATGAATACACAAAGTAACAT 650

RESULT 15
AAN60490
ID AAN60490 standard; mRNA; 622 BP.
XX
XX AAN60490;

```
XX 03-OCT-2002 (updated)
DT 31-JUL-1991 (first entry)
XX Human prepro-somatomedin-C.
XX Somatomedin-C; ss.
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 3..360
FT /*tag= a
FT /label= prepro-somatomedin-C
FT mat_peptide 45..254
FT /*tag= b
FT /label= mature somatomedin-C
XX
XX MO8600619-A.
XX 30-JAN-1986.
XX
XX 10-JUL-1985: 85WO-US01325.
XX
XX 13-JUL-1984: 84US-0630557.
XX
XX (CHIR-) CHIRON CORP.
XX
XX Bell G, Rail LB, Merryweather JP:
XX WPI: 1986-042104/05.
XX P-PSDB: AAP60578.
XX
XX Pre:pro insulin-like growth factors I and II - obtd. from the
XX human genome by e.g. screening a cDNA library obtd. from human
XX liver cells.
XX
XX PS Disclosure; Fig 1; 20pp; English.
XX
XX CC The sequence, derived from plasmid phage phigfl, encodes human
XX prepro-somatomedin-C. The sequence may be used for hormone
XX production, and is useful for the preparation of DNA probes to
XX detect the presence of the genes in a natural source. The probes
XX CC may be used to detect mutations and/or deletions in humans
XX suffering from growth deficiencies.
XX See also AA060489, AA060491
XX CC (Updated on 03-OCT-2002 to add missing OS field.)
XX
SQ Sequence 622 BP; 171 A; 147 C; 161 G; 143 U; 0 other;

Query Match 65.6%; Score 339.4; DB 7; Length 622;
Best Local Similarity 69.7%; Pred. No. 1.3e-92;
Matches 363; Conservative 89; Mismatches 16; Indels 53; Gaps 5;

QY 1 GGACCGAGAGCGCTCTGCGGGGCTGAGCTGATGCTCTCAGTTCGTGTGTGAGAC 60
Db 45 GGACCGAGAGCGCTCTGCGGGGCTGAGCTGATGCTCTCAGTTCGTGTGTGAGAC 104
QY 61 AGGGGCTTTATTCAACAAGCCACAGGGTATGGCTCCAGCATGTGGAGGGCCCTCAG 120
Db 105 AGGGGCTTTATTCAACAAGCCACAGGGTATGGCTCCAGCATGTGGAGGGCCCTCAG 164
QY 121 ACAGGATCGTGTAGTATGCTCTCCGAGCTGTGATCTAAGAGAGCTGAGATGTAT 180
Db 165 ACAGGATCGTGTAGTATGCTCTCCGAGCTGTGATCTAAGAGAGCTGAGATGTAT 224
QY 181 TCGGCACCCCTCAAGCTGCGCAAGTACGCTCGCTGTCCGTGCCACGCGCACGAC 240
Db 225 UCGCACCCCTCAAGCTGCGCAAGTACGCTCGCTGTCCGTGCCACGCGCACGAC 284
QY 241 ATGCCCAAGACCAAGATATCAGCCCATCTACCAACAAGAACGAAAGTCTCAGAGA 300
Db 285 AUGCCCAAGACCCAG----- 299
```

```
QY 301 AGGAAGGAGTACTATTGAAGAACACAGTAGAGGGAGTGCAGGAAACAAGAACTACG 360
Db 300 ----AAGGAGUACAUUUGAAGAACGCAAGUGAGGGAGUGCAGGAAACAAGAACTACG 355
QY 361 GATGTA-GAAGACCCCTTCTGAGAGTGAAGAAGACAGCCACGCGAGACCTTGTCTC 419
Db 356 GAUGTAGAAGAACCCCTTCTGAGAGTGAAGAAGACAGCCACGCGAGACCTTGTCTC 415
QY 420 TGCAC-AGTTACCTG-TAACATTGGANTACGGGCCAAAAAATAAGTTGATCATTTTC 477
Db 416 UGCACGAGUUAACUGUUAACUUGGAAACCCUACCAAAAAAUAAGUUGAUAACAUUA 475
QY 478 AAGAT-GGCATTTCCCAATGAATACACAAGTAAACAT 517
Db 476 AAGAGGGGCGUUCGCCCAAUAGAAUACACAAGUAAACAU 516
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Search completed: June 15, 2003, 16:08:47
Job time : 160.835 secs

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OM nucleic - nucleic search, using sw model

Run on: June 15, 2003, 15:46:38 ; Search time 41.9101 Seconds
(without alignments)
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Title: US-09-852-261-1

Perfect score: 517

Sequence: 1 ggaacgagagcgtctgcg.....tgaatcaccaagaataacat 517

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database :

- Issued Patents NA:*
- 1: /cgn2_6/prodata/2/ina/5A_COMB.seq:*
 - 2: /cgn2_6/prodata/2/ina/5B_COMB.seq:*
 - 3: /cgn2_6/prodata/2/ina/6A_COMB.seq:*
 - 4: /cgn2_6/prodata/2/ina/6B_COMB.seq:*
 - 5: /cgn2_6/prodata/2/ina/PCTUS_COMB.seq:*
 - 6: /cgn2_6/prodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------------|
| 1 | 467.4 | 90.4 | 553 | 4 | US-09-142-583A-3 |
| 2 | 467.4 | 90.4 | 553 | 4 | US-09-142-583A-5 |
| 3 | 342.6 | 66.3 | 777 | 4 | US-09-142-583A-10 |
| 4 | 339.4 | 65.6 | 622 | 6 | 5405942-2 |
| 5 | 286.4 | 55.4 | 5707 | 2 | US-08-472-809B-8 |
| 6 | 286.4 | 55.4 | 6345 | 2 | US-08-472-809B-7 |
| 7 | 285.2 | 49.4 | 357 | 6 | 5405942-13 |
| 8 | 253.6 | 49.1 | 357 | 6 | 5405942-9 |
| 9 | 208.4 | 40.3 | 210 | 6 | 5405942-11 |
| 10 | 208.4 | 40.3 | 210 | 6 | 5405942-11 |
| 11 | 208.4 | 40.3 | 2862 | 4 | US-09-255-829-13 |
| 12 | 206.8 | 40.0 | 210 | 6 | 5405942-15 |
| 13 | 202.8 | 39.2 | 240 | 1 | US-08-308-196A-1 |
| 14 | 202.8 | 39.2 | 240 | 5 | PCT-US91-06452-1 |
| 15 | 202.8 | 39.2 | 390 | 3 | US-09-029-267-13 |
| 16 | 174.4 | 33.7 | 798 | 1 | US-07-953-230A-6 |
| 17 | 163.4 | 31.6 | 770 | 1 | US-07-953-230A-1 |
| 18 | 163.4 | 31.6 | 846 | 1 | US-07-953-230A-5 |
| 19 | 125.8 | 24.3 | 485 | 1 | US-07-989-845-29 |
| 20 | 125.8 | 24.3 | 485 | 1 | US-07-989-844-13 |
| 21 | 125.8 | 24.3 | 485 | 1 | US-08-110-663-1 |
| 22 | 125.8 | 24.3 | 485 | 1 | US-08-169-688-1 |
| 23 | 125.8 | 24.3 | 485 | 1 | US-08-240-121-13 |
| 24 | 125.8 | 24.3 | 485 | 1 | US-08-451-241-13 |
| 25 | 125.8 | 24.3 | 485 | 1 | US-08-110-664-1 |
| 26 | 125.8 | 24.3 | 485 | 1 | US-08-446-882-1 |
| 27 | 125.8 | 24.3 | 485 | 1 | US-08-385-187A-1 |

| | | | | | | |
|----|-------|------|-----|---|-------------------|-------------------|
| 28 | 125.8 | 24.3 | 485 | 1 | US-08-470-108-1 | Sequence 1, Appl |
| 29 | 125.8 | 24.3 | 485 | 5 | PCT-US93-11287-13 | Sequence 13, Appl |
| 30 | 125.8 | 24.3 | 485 | 5 | PCT-US93-11288-29 | Sequence 29, Appl |
| 31 | 123.8 | 23.9 | 621 | 3 | US-08-989-251-40 | Sequence 40, Appl |
| 32 | 123.8 | 23.9 | 621 | 3 | US-09-340-250-40 | Sequence 40, Appl |
| 33 | 123.8 | 23.9 | 621 | 4 | US-09-528-108-40 | Sequence 40, Appl |
| 34 | 122 | 23.6 | 237 | 1 | US-07-764-655D-8 | Sequence 8, Appl |
| 35 | 120.8 | 23.3 | 243 | 2 | US-08-482-183-75 | Sequence 75, Appl |
| 36 | 120.4 | 23.3 | 233 | 1 | US-08-444-143-3 | Sequence 3, Appl |
| 37 | 120.4 | 23.3 | 233 | 1 | US-07-764-655D-9 | Sequence 9, Appl |
| 38 | 120.4 | 23.3 | 237 | 1 | US-08-284-784-40 | Sequence 40, Appl |
| 39 | 120.4 | 23.3 | 717 | 2 | US-08-854-811-40 | Sequence 40, Appl |
| 40 | 120.4 | 23.3 | 717 | 2 | US-08-854-811-40 | Sequence 43, Appl |
| 41 | 120.4 | 23.3 | 783 | 2 | US-08-284-784-43 | Sequence 43, Appl |
| 42 | 120.4 | 23.3 | 783 | 2 | US-08-854-811-43 | Sequence 33, Appl |
| 43 | 120.4 | 23.3 | 891 | 1 | US-08-284-784-34 | Sequence 34, Appl |
| 44 | 120.4 | 23.3 | 891 | 1 | US-08-854-811-33 | Sequence 33, Appl |
| 45 | 120.4 | 23.3 | 891 | 2 | US-08-854-811-33 | Sequence 33, Appl |

ALIGNMENTS

RESULT 1
US-09-142-583A-3
Sequence 3, Application US/09142583A
Patent No. 6221842
GENERAL INFORMATION:
APPLICANT: GOLDSPIK, GEOFREY
TITLE OF INVENTION: METHOD OF TREATING MUSCULAR DISORDERS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P. C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/142,583A
FILING DATE: 29-Oct-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB97/00658
FILING DATE: 11-MAR-1997
APPLICATION NUMBER: GB 9605124.8
FILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B. J.
REGISTRATION NUMBER: 36663
REFERENCE/DOCKET NUMBER: 117-263
TELECOMMUNICATION INFORMATION:
TELEPHONE: 7038164000
TELEFAX: 7038164100
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..363
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-142-583A-3
Query Match 90.4%; Score 467.4; DB 4; Length 553;

Best Local Similarity 96.2%; Pred. No. 1,2e-134;
Matches 501; Conservative 0; Mismatches 16; Indels 4; Gaps 2;

QY 1 GCACCGGAGACGCTTGGGGGGGAGAGTGTGATGCTCTTCACTTGTGTGGAGAC 60
DB 31 GCACCGGAGACGCTTGGGGGGGAGAGTGTGATGCTCTTCACTTGTGTGGAGAC 90
QY 61 AGGGGCTTTTATTCAACAGAGCCGAGAGTGTGATGCTCTTCACTTGTGTGGAGAC 120
DB 91 AGGGGCTTTTATTCAACAGAGCCGAGAGTGTGATGCTCTTCACTTGTGTGGAGAC 150
QY 121 ACAGGCTGTGTGATGCTCTTCACTTGTGTGGAGTGTGATGCTCTTCACTTGTGTGGAGAC 180
DB 151 ACAGGCTGTGTGATGCTCTTCACTTGTGTGGAGTGTGATGCTCTTCACTTGTGTGGAGAC 210
QY 181 TGGGACCCCTCAACGCTTGGGGGGGAGAGTGTGATGCTCTTCACTTGTGTGGAGAC 240
DB 211 TGGGACCCCTCAACGCTTGGGGGGGAGAGTGTGATGCTCTTCACTTGTGTGGAGAC 270
QY 241 ATGCCCAAGACCCAGAGTATCAGCCCTTCACTTCAACAGAGAGAGAGAGTGTGATGCTCTTCACTTGTGTGGAGAC 297
DB 271 ATGCCCAAGACCCAGAGTATCAGCCCTTCACTTCAACAGAGAGAGAGAGTGTGATGCTCTTCACTTGTGTGGAGAC 330
QY 298 AGAAGGAAAGAGAGTGTGATGCTCTTCACTTCAACAGAGAGAGAGAGTGTGATGCTCTTCACTTGTGTGGAGAC 357
DB 331 AGAAGGAAAGAGAGTGTGATGCTCTTCACTTCAACAGAGAGAGAGAGTGTGATGCTCTTCACTTGTGTGGAGAC 390
QY 358 CAGATGTA-GAAGACCCCTTGGAGAGTGTGATGCTCTTCACTTCAACAGAGAGAGAGTGTGATGCTCTTCACTTGTGTGGAGAC 416
DB 391 CAGATGTA-GAAGACCCCTTGGAGAGTGTGATGCTCTTCACTTCAACAGAGAGAGAGTGTGATGCTCTTCACTTGTGTGGAGAC 450
QY 417 CTCTGCACAGTGTGATGCTCTTCACTTCAACAGAGAGAGAGTGTGATGCTCTTCACTTGTGTGGAGAC 476
DB 451 CTCTGCACAGTGTGATGCTCTTCACTTCAACAGAGAGAGAGTGTGATGCTCTTCACTTGTGTGGAGAC 510
QY 477 CAAGATGCAATTTCCCAATGAATACAGTAACAT 517
DB 511 CAAGATGCAATTTCCCAATGAATACAGTAACAT 551

RESULT 2

US-09-142-583A-5
Sequence 5, Application US/09142583A
Patent No. 6221842

GENERAL INFORMATION:

APPLICANT: GOLDSPIRK, GEOFFREY
TITLE OF INVENTION: METHOD OF TREATING MUSCULAR DISORDERS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22201

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/142,583A
FILING DATE: 29-Oct-1998
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/GB97/00658
FILING DATE: 11-MAR-1997
APPLICATION NUMBER: GB 9605124.8
FILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B. J.
REGISTRATION NUMBER: 36663
REFERENCE/DOCKET NUMBER: 11-263

TELECOMMUNICATION INFORMATION:

TELEPHONE: 7038164000
TELEFAX: 7038164100

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
LENGTH: 553 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: Linear
MOLECULE TYPE: cDNA
FEATURE:

NAME/KEY: CDS
LOCATION: 341..397

US-09-142-583A-5
SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Query Match 90.4%; Score 467.4; DB 4; Length 553;
Best Local Similarity 96.2%; Pred. No. 1,2e-134;
Matches 501; Conservative 0; Mismatches 16; Indels 4; Gaps 2;

QY 1 GSAACCGGAGACGCTTGGGGGGGAGAGTGTGATGCTCTTCACTTGTGTGGAGAC 60
DB 31 GCACCGGAGACGCTTGGGGGGGAGAGTGTGATGCTCTTCACTTGTGTGGAGAC 90
QY 61 AGGGGCTTTTATTCAACAGAGCCGAGAGTGTGATGCTCTTCACTTGTGTGGAGAC 120
DB 91 AGGGGCTTTTATTCAACAGAGCCGAGAGTGTGATGCTCTTCACTTGTGTGGAGAC 150
QY 121 ACAGGCTGTGTGATGCTCTTCACTTGTGTGGAGTGTGATGCTCTTCACTTGTGTGGAGAC 180
DB 151 ACAGGCTGTGTGATGCTCTTCACTTGTGTGGAGTGTGATGCTCTTCACTTGTGTGGAGAC 210
QY 181 TGGGACCCCTCAACGCTTGGGGGGGAGAGTGTGATGCTCTTCACTTGTGTGGAGAC 240
DB 211 TGGGACCCCTCAACGCTTGGGGGGGAGAGTGTGATGCTCTTCACTTGTGTGGAGAC 270
QY 241 ATGCCCAAGACCCAGAGTATCAGCCCTTCACTTCAACAGAGAGAGAGTGTGATGCTCTTCACTTGTGTGGAGAC 297
DB 271 ATGCCCAAGACCCAGAGTATCAGCCCTTCACTTCAACAGAGAGAGAGTGTGATGCTCTTCACTTGTGTGGAGAC 330
QY 298 AGAAGGAAAGAGAGTGTGATGCTCTTCACTTCAACAGAGAGAGAGAGTGTGATGCTCTTCACTTGTGTGGAGAC 357
DB 331 AGAAGGAAAGAGAGTGTGATGCTCTTCACTTCAACAGAGAGAGAGAGTGTGATGCTCTTCACTTGTGTGGAGAC 390
QY 358 CAGATGTA-GAAGACCCCTTGGAGAGTGTGATGCTCTTCACTTCAACAGAGAGAGAGTGTGATGCTCTTCACTTGTGTGGAGAC 416
DB 391 CAGATGTA-GAAGACCCCTTGGAGAGTGTGATGCTCTTCACTTCAACAGAGAGAGAGTGTGATGCTCTTCACTTGTGTGGAGAC 450
QY 417 CTCTGCACAGTGTGATGCTCTTCACTTCAACAGAGAGAGAGTGTGATGCTCTTCACTTGTGTGGAGAC 476
DB 451 CTCTGCACAGTGTGATGCTCTTCACTTCAACAGAGAGAGAGTGTGATGCTCTTCACTTGTGTGGAGAC 510
QY 477 CAAGATGCAATTTCCCAATGAATACAGTAACAT 517
DB 511 CAAGATGCAATTTCCCAATGAATACAGTAACAT 551

RESULT 3

US-09-142-583A-10
Sequence 10, Application US/09142583A
Patent No. 6221842

GENERAL INFORMATION:

APPLICANT: GOLDSPIRK, GEOFFREY
TITLE OF INVENTION: METHOD OF TREATING MUSCULAR DISORDERS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22201

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/142,583A
FILING DATE: 29-Oct-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB97/00658
FILING DATE: 11-MAR-1997
APPLICATION NUMBER: GB 9605124.8
FILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B. J.
REGISTRATION NUMBER: 36663
REFERENCE/DOCKET NUMBER: 117-263
TELECOMMUNICATION INFORMATION:
TELEPHONE: 7038164000
TELEFAX: 7038164100
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 777 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 26..493
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-142-583A-10

Query Match 66.3%; Score 342.6; DB 4; Length 777;
Best Local Similarity 87.1%; Pred. No. 3.8e-96;
Matches 454; Conservative 0; Mismatches 14; Indels 53; Gaps 5;

1 GGACCGGAGAGCGCTCGGGGCTGAGCTGATGATCTCTTCAAGTTCGTTGAGGAGAC 60
179 GGACCGGAGAGCGCTCGGGGCTGAGCTGATGATCTCTTCAAGTTCGTTGAGGAGAC 238
61 AGGGGCTTTTATTTCACAAGCCGACAGGATGCTCCAGAGTCGGAGGGCGCTCAG 120
239 AGGGGCTTTTATTTCACAAGCCGACAGGATGCTCCAGAGTCGGAGGGCGCTCAG 288
121 ACAGGATCGTGGATGAGTGTCTGCTCCGAGCGTGTATCTAAGAGAGCTGGAGATGAT 180
299 ACAGGATCGTGGATGAGTGTCTGCTCCGAGCGTGTATCTAAGAGAGCTGGAGATGAT 358
181 TGGCGACCCCTCAAGCCTGCGCAAGTCAGTCTGCTGCTCCGCGCCAGCGCCACCGAG 240
359 TGGCGACCCCTCAAGCCTGCGCAAGTCAGTCTGCTGCTCCGCGCCAGCGCCACCGAG 418
241 ATGGCCCAAGACCGAAGTATCAAGCCCCCATCTACCAAGAACAGCAAGTCTCAGAGA 300
419 ATGGCCCAAGACCGAAGTATCAAGCCCCCATCTACCAAGAACAGCAAGTCTCAGAGA 433
301 AGGAAGAAGATGATTTGAAGAACACAGTAGAGGAGTGCAGAAACAGAACTACAG 360
434 AAGGAAGTACATTTGAAGAACAGCAAGTAGAGGAGTGCAGAAACAGAACTACAG 489
361 GATGTA-GAAGACCCCTCTGAGAGTGAAGAGACAGGCCACCGACGACCTTTGCTC 419
490 GATGTAAGAGAGCCCTCTGAGAGTGAAGAGTGAAGTGCACCGACGAGTCTTGTCTC 549
420 TGCAC-AGTTACTG-TAAACATTGGAATACGGCCAAAATAAGTTTATACATTTC 477
550 TGCACAGGTTACTGTTAACTTTGGAGACACCTACCAAAAAATTAAGTTTATACATTTC 609
478 AAGGAT-GGCAATTCGCCCAATGAATATACCAAGTAAACAT 517
610 AAGGATGGCGTTCCCGCAATGAATATACCAAGTAAACAT 650

RESULT 4
5405942-2
Patent No. 5405942
APPLICANT: BELT, GRAEME I.; FALL, LESLIE B.; MERRYWEATHER,
JAMES P.
TITLE OF INVENTION: PREPRO INSULIN-LIKE GROWTH FACTORS
I AND II
NUMBER OF SEQUENCES: 16
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/65,673
FILING DATE: 16-JUN-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 630,557
FILING DATE: 19-JUL-1984
SEQ ID NO: 2
LENGTH: 622
5405942-2

Query Match 65.6%; Score 339.4; DB 6; Length 622;
Best Local Similarity 69.7%; Pred. No. 3.4e-95;
Matches 363; Conservative 89; Mismatches 16; Indels 53; Gaps 5;

1 GGACCGGAGAGCGCTCGGGGCTGAGCTGATGATCTCTTCAAGTTCGTTGAGGAGAC 60
45 GGACCGGAGAGCGCTCGGGGCTGAGCTGATGATCTCTTCAAGTTCGTTGAGGAGAC 104
61 AGGGGCTTTTATTTCACAAGCCGACAGGATGCTCCAGAGTCGGAGGGCGCTCAG 120
105 AGGGGCTTTTATTTCACAAGCCGACAGGATGCTCCAGAGTCGGAGGGCGCTCAG 164
121 ACAGGATCGTGGATGAGTGTCTGCTCCGAGCGTGTATCTAAGAGAGCTGGAGATGAT 180
165 ACAGGATCGTGGATGAGTGTCTGCTCCGAGCGTGTATCTAAGAGAGCTGGAGATGAT 224
181 TGGCGACCCCTCAAGCCTGCGCAAGTCAGTCTGCTGCTCCGCGCCAGCGCCACCGAG 240
225 TGGCGACCCCTCAAGCCTGCGCAAGTCAGTCTGCTGCTCCGCGCCAGCGCCACCGAG 284
241 ATGGCCCAAGACCGAAGTATCAAGCCCCCATCTACCAAGAACAGCAAGTCTCAGAGA 300
285 ATGGCCCAAGACCGAAGTATCAAGCCCCCATCTACCAAGAACAGCAAGTCTCAGAGA 299
301 AGGAAGAAGATGATTTGAAGAACACAGTAGAGGAGTGCAGAAACAGAACTACAG 360
300 AAGGAAGTACATTTGAAGAACAGCAAGTAGAGGAGTGCAGAAACAGAACTACAG 355
361 GATGTA-GAAGACCCCTCTGAGAGTGAAGAGACAGGCCACCGACGACCTTTGCTC 419
356 GAUGUAGAGAGACCCCTCTGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 415
420 TGCAC-AGTTACTG-TAAACATTGGAATACGGCCAAAATAAGTTTATACATTTC 477
416 USCACAGAGUACCCUUGUAAACUUGUAAACUUGUAAACUUGUAAACUUGUAAACUUGA 475
478 AAGGAT-GGCAATTCGCCCAATGAATATACCAAGTAAACAT 517
476 AAGGATGGCGTTCCCGCAATGAATATACCAAGTAAACAT 516

RESULT 5
US-08-472-809B-8
Sequence 8, Application US/08472809B
Patent No. 5925564
GENERAL INFORMATION:
APPLICANT: Schwartz, Robert J.
APPLICANT: DeMayo, Franco J.
APPLICANT: O'Malley, Bert W.
TITLE OF INVENTION: Expression Vector Systems and
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSER: Lyon & Lyon

```

STREET: 633 West Fifth Street
STREET: Suite 4700
City: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,809B
FILING DATE: June 7, 1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/209,846
FILING DATE: March 9, 1994
APPLICATION NUMBER: 07/789,919
FILING DATE: No. 5925564ember 6, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Marburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 214/212
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ. ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 5707 bases
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-472-809B-8

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Query Match 55.4%; Score 286.4; DB 2; Length 5707;
Best Local Similarity 85.6%; Pred. No. 1.9e-78;
Matches 363; Conservative 0; Mismatches 11; Indels 50; Gaps 2;

1 GGACCGGAGAGCGCTGCGGGGCTGAGTGGATGCTCTCAGTGTGTGGAGAC 60
793 GGACCGGAGAGCGCTGCGGGGCTGAGTGGATGCTCTCAGTGTGTGGAGAC 852
61 AGGGGCTTTTATTTCACAAAGCCACAGGGTATGGCTCCAGCAGTCCGAGGCGCCTCAG 120
853 AGGGGCTTTTATTTCACAAAGCCACAGGGTATGGCTCCAGCAGTCCGAGGCGCCTCAG 912
121 ACAGGATGCTGATAGTGTGCTCCGAGCTGTGATCTAAGAGAGTGTGATAT 180
913 ACAGGATGCTGATAGTGTGCTCCGAGCTGTGATCTAAGAGAGTGTGATAT 972
181 TGCGCACCCCTCAAGGCTGCCAAGTCAGCTGCTGTCGCCAGGCCACACCGAC 240
973 TGCGCACCCCTCAAGGCTGCCAAGTCAGCTGCTGTCGCCAGGCCACACCGAC 1032
241 ATGCCCAAGACCCAGAGATATCAGCCCCCATCTACCAAGAAACAGCAAGTCTCAGAGA 300
1033 ATGCCCAAGACCCAG----- 1047
301 AGGAAGAGAGTCAATTTGAAGACAGAGTAGAGAGTGCAGAAACAGATACAG 360
1048 ----AGGAAGATCAATTTGAAGACAGAGTAGAGAGTGCAGAAACAGATACAG 1103
361 GATGTA-GAAGACCCCTTGTGAGAGTGAAGAAAGACAGGCCACCGAGAGACCTTTGCTC 419
1104 GATGTGAGAGAGACCCCTTGTGAGAGTGAAGAAAGATGATGATCCAGCCGAGAGATCCCGCGGC 1163
420 TGCA 423
1164 TGCA 1167

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RESULT 6
US-08-472-809B-7
Sequence 7, Application US/08472809B
Patent No. 5925564
GENERAL INFORMATION:
APPLICANT: Schwartz, Robert J.
APPLICANT: Demayo, Franco J.
APPLICANT: O'Malley, Bert W.
TITLE OF INVENTION: Expression Vector Systems and
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
City: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,809B
FILING DATE: June 7, 1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/209,846
FILING DATE: March 9, 1994
APPLICATION NUMBER: 07/789,919
FILING DATE: No. 5925564ember 6, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Marburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 214/212
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ. ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 6345 bases
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-472-809B-7

Query Match 55.4%; Score 286.4; DB 2; Length 6345;
Best Local Similarity 85.6%; Pred. No. 2e-78;
Matches 363; Conservative 0; Mismatches 11; Indels 50; Gaps 2;

1 GGACCGGAGAGCGCTGCGGGGCTGAGTGGATGCTCTCAGTGTGTGGAGAC 60
3702 GGACCGGAGAGCGCTGCGGGGCTGAGTGGATGCTCTCAGTGTGTGGAGAC 3761
61 AGGGGCTTTTATTTCACAAAGCCACAGGGTATGGCTCCAGCAGTCCGAGGCGCCTCAG 120
3762 AGGGGCTTTTATTTCACAAAGCCACAGGGTATGGCTCCAGCAGTCCGAGGCGCCTCAG 3821
121 ACAGGATGCTGATAGTGTGCTCCGAGCTGTGATCTAAGAGAGTGTGATAT 180
3822 ACAGGATGCTGATAGTGTGCTCCGAGCTGTGATCTAAGAGAGTGTGATAT 3881
181 TGCGCACCCCTCAAGGCTGCCAAGTCAGCTGCTGTCGCCAGGCCACACCGAC 240
3882 TGCGCACCCCTCAAGGCTGCCAAGTCAGCTGCTGTCGCCAGGCCACACCGAC 3941

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JAMES P.
TITLE OF INVENTION: PREPRO INSULIN-LIKE GROWTH FACTORS
I AND II
NUMBER OF SEQUENCES: 16
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/65,673
FILING DATE: 16-JUN-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 630,557
FILING DATE: 19-JUL-1984
SEQ ID NO:11:
LENGTH: 210
5405942-11
Query Match 40.3%; Score 208.4; DB 6; Length 210;
Best Local Similarity 99.5%; Pred. No. 4.8e-55;
Matches 209; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGACCGGAGAGCGCTCTGCGGGGCTGAGCTGTGTGATGCTCTTCAGTTGCTGTGTGAGAC 60
DB 1 GGACCGGAGAGCGCTCTGCGGGGCTGAGCTGTGTGATGCTCTTCAGTTGCTGTGTGAGAC 60
QY 61 AGGGGCTTTTATTTCACAAAGCCACAGGGTATGCTCCAGCGAGTGGAGGGGCGCTCAG 120
DB 61 AGGGGCTTTTATTTCACAAAGCCACAGGGTATGCTCCAGCGAGTGGAGGGGCGCTCAG 120
QY 121 ACAGCATGCTGTGATGAGTGTCTGCTTCCGAGGCTGTATCTAAGAGGCTGTGAGATGTAT 180
DB 121 ACAGCATGCTGTGATGAGTGTCTGCTTCCGAGGCTGTATCTAAGAGGCTGTGAGATGTAT 180
QY 181 TGCGCACCCCTCAAGCTGTGCAAGTCAGCT 210
DB 181 TGCGCACCCCTCAAGCTGTGCAAGTCAGCT 210
RESULT 11
US-09-829-13
Sequence 13, Application US/09255829
Patent No. 6461617
GENERAL INFORMATION:
APPLICANT: Shone, Clifford Charles
APPLICANT: Quinn, Conrad Padraig
APPLICANT: Foster, Keith Alan
TITLE OF INVENTION: Recombinant Toxin Fragments
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN, & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/255,829
FILING DATE: 23-FEB-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB97/02273
FILING DATE: 22-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/782,893
FILING DATE: 27-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: ESMOND, ROBERT W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1581.0130002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 2862 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2862
US-09-829-13
Query Match 40.3%; Score 208.4; DB 4; Length 2862;
Best Local Similarity 99.5%; Pred. No. 1.5e-54;
Matches 209; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGACCGGAGAGCGCTCTGCGGGGCTAGCTGTGTGATGCTCTTCAGTTGCTGTGTGAGAC 60
DB 2644 GGACCGGAGAGCGCTCTGCGGGGCTAGCTGTGTGATGCTCTTCAGTTGCTGTGTGAGAC 2703
QY 61 AGGGGCTTTTATTTCACAAAGCCACAGGGTATGCTCCAGCGAGTGGAGGGGCGCTCAG 120
DB 2704 AGGGGCTTTTATTTCACAAAGCCACAGGGTATGCTCCAGCGAGTGGAGGGGCGCTCAG 2763
QY 121 ACAGCATGCTGTGATGAGTGTCTGCTTCCGAGGCTGTATCTAAGAGGCTGTGAGATGTAT 180
DB 2764 ACAGCATGCTGTGATGAGTGTCTGCTTCCGAGGCTGTATCTAAGAGGCTGTGAGATGTAT 2823
QY 181 TGCGCACCCCTCAAGCTGTGCAAGTCAGCT 210
DB 2824 TGCGCACCCCTCAAGCTGTGCAAGTCAGCT 2853
RESULT 12
5405942-15
Patent No. 5405942
APPLICANT: BELL, GRAEME I.; RALL, LESLIE B.; MERRYWEATHER,
JAMES P.
TITLE OF INVENTION: PREPRO INSULIN-LIKE GROWTH FACTORS
I AND II
NUMBER OF SEQUENCES: 16
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/65,673
FILING DATE: 16-JUN-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 630,557
FILING DATE: 19-JUL-1984
SEQ ID NO:15:
LENGTH: 210
5405942-15
Query Match 40.0%; Score 206.8; DB 6; Length 210;
Best Local Similarity 77.1%; Pred. No. 1.5e-54;
Matches 162; Conservative 46; Mismatches 2; Indels 0; Gaps 0;
QY 1 GGACCGGAGAGCGCTCTGCGGGGCTGAGCTGTGTGATGCTCTTCAGTTGCTGTGTGAGAC 60
DB 1 GGACCGGAGAGCGCTCTGCGGGGCTGAGCTGTGTGATGCTCTTCAGTTGCTGTGTGAGAC 60
QY 61 AGGGGCTTTTATTTCACAAAGCCACAGGGTATGCTCCAGCGAGTGGAGGGGCGCTCAG 120
DB 61 AGGGGCTTTTATTTCACAAAGCCACAGGGTATGCTCCAGCGAGTGGAGGGGCGCTCAG 120
QY 121 ACAGCATGCTGTGATGAGTGTCTGCTTCCGAGGCTGTATCTAAGAGGCTGTGAGATGTAT 180
DB 121 ACAGCATGCTGTGATGAGTGTCTGCTTCCGAGGCTGTATCTAAGAGGCTGTGAGATGTAT 180
QY 181 TGCGCACCCCTCAAGCTGTGCAAGTCAGCT 210
DB 181 TGCGCACCCCTCAAGCTGTGCAAGTCAGCT 210
RESULT 13


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Sequence 13: Application US/09029267
Patent No. 6107057
GENERAL INFORMATION:
APPLICANT: Crawford, Kenneth
APPLICANT: Zador, Isabel
APPLICANT: Innis, Michael
TITLE OF INVENTION: Pichia Secretary Leader for Protein
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: California
COUNTRY: United States
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/029,267
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Chung, Ling-Fong
REGISTRATION NUMBER: 36,482
REFERENCE/DOCKET NUMBER: 1165.100
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2704
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 390 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Synthetic"
US-09-029-267-13

Query Match      39.2%  Score 202.8: DB 3: Length 390;
Best Local Similarity 96.7%  Pred. No. 3.3e-53;
Matches 207; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 GGACCGGAGACGCTGCGGGGCTGAGCTGTGATGCTCTTCAGTTCTGTGTGAGAC 60
DB 160 GGACCGGAGACGCTGCGGGGCTGAGCTGTGATGCTCTTCAGTTCTGTGTGAGAC 219
QY 61 AGGGGCTTTATTTCAACAAGCCACAGGGTATGCTCCAGCAGTCGGAGGGCGCTCAG 120
DB 220 AGGGGCTTTATTTCAACAAGCCACAGGGTATGCTCCAGCAGTCGGAGGGCGCTCAG 279
QY 121 ACAGGATGATGATGATGATGCTCTCCGAGCTGTATTAAGAGAGCTGAGATGAT 180
DB 280 ACAGGATGATGATGATGATGCTCTCCGAGCTGTATTAAGAGAGCTGAGATGAT 339
QY 181 TCGCAGACCCCTCAAGCTGCGAAGTCAGCTCGCT 214
DB 340 TCGCAGACCCCTCAAGCTGCGAAGTCAGCTCGCT 373
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Search completed: June 15, 2003, 18:20:40
Job time : 43.9101 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 15, 2003, 17:22:19 ; Search time 93 6428 Seconds
(without alignments)
7994.713 Million cell updates/sec

Title: US-09-852-261-1

Perfect score: 517

Sequence: 1 ggaacgagagagcgtctgcg.....tgaataacacagtaaacat 517

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 1029858 seqs, 724030393 residues

Total number of hits satisfying chosen parameters: 2059716

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_NA:*

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- 2: /cgn2_6/ptodata/2/pubpna/PCR_NEW.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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- 6: /cgn2_6/ptodata/2/pubpna/PCRUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
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- 11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
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- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 517 | 100.0 | 517 | 10 | US-09-852-261-1 |
| 2 | 467.4 | 90.4 | 523 | 10 | US-09-852-261-5 |
| 3 | 377.2 | 73.0 | 471 | 10 | US-09-852-261-13 |
| 4 | 344.2 | 66.6 | 7260 | 9 | US-10-136-639-4 |
| 5 | 344.2 | 66.6 | 7260 | 10 | US-09-819-497-24 |
| 6 | 344.2 | 66.6 | 7260 | 10 | US-09-880-107-3739 |
| 7 | 325.2 | 62.9 | 539 | 9 | US-09-852-261-3 |
| 8 | 318.2 | 61.5 | 651 | 9 | US-10-161-088-1 |
| 9 | 258.4 | 50.0 | 318 | 10 | US-09-852-261-9 |
| 10 | 247.8 | 47.9 | 487 | 10 | US-09-852-261-11 |
| 11 | 228 | 44.1 | 462 | 9 | US-10-238-114-1 |
| 12 | 204.6 | 39.6 | 4532 | 10 | US-09-830-3778-1 |
| 13 | 203.6 | 39.4 | 210 | 10 | US-09-930-3778-2 |
| 14 | 202.8 | 39.2 | 390 | 9 | US-10-179-046-13 |
| 15 | 202 | 39.1 | 286 | 9 | US-10-161-088-3 |
| 16 | 140.2 | 27.1 | 213 | 9 | US-10-076-816-9 |
| 17 | 140.2 | 27.1 | 213 | 9 | US-10-077-381-9 |
| 18 | 123.8 | 23.9 | 621 | 9 | US-10-280-826-40 |
| 19 | 123.8 | 23.9 | 621 | 10 | US-09-921-398-40 |

| | | | | | | |
|----|-------|------|------|----|--------------------|--------------------|
| 20 | 108.6 | 21.0 | 480 | 9 | US-10-280-826-38 | Sequence 38, Appl |
| 21 | 108.6 | 21.0 | 480 | 10 | US-09-921-398-38 | Sequence 38, Appl |
| 22 | 75.4 | 14.6 | 411 | 10 | US-09-960-352-2082 | Sequence 2082, Ap |
| 23 | 72.4 | 14.0 | 854 | 9 | US-09-954-531-989 | Sequence 989, App |
| 24 | 71.8 | 13.9 | 237 | 9 | US-10-136-841-3 | Sequence 3, Appl |
| 25 | 70.6 | 13.7 | 447 | 9 | US-10-025-380-917 | Sequence 917, App |
| 26 | 70.6 | 13.7 | 447 | 10 | US-09-922-217-917 | Sequence 917, App |
| 27 | 70.6 | 13.7 | 447 | 10 | US-09-833-263-917 | Sequence 917, App |
| 28 | 70.4 | 13.6 | 437 | 9 | US-10-066-543-663 | Sequence 663, App |
| 29 | 70.4 | 13.6 | 433 | 9 | US-10-066-543-997 | Sequence 997, App |
| 30 | 70.4 | 13.6 | 518 | 9 | US-10-066-543-1040 | Sequence 1040, Ap |
| 31 | 70.4 | 13.6 | 536 | 9 | US-10-066-543-428 | Sequence 428, Appl |
| 32 | 70.4 | 13.6 | 543 | 9 | US-10-136-841-1 | Sequence 1, Appl |
| 33 | 70.4 | 13.6 | 549 | 9 | US-10-066-543-478 | Sequence 478, App |
| 34 | 70.4 | 13.6 | 574 | 9 | US-10-025-380-918 | Sequence 918, App |
| 35 | 70.4 | 13.6 | 574 | 10 | US-09-922-217-918 | Sequence 918, App |
| 36 | 70.4 | 13.6 | 574 | 10 | US-09-833-263-918 | Sequence 918, App |
| 37 | 70.4 | 13.6 | 577 | 9 | US-10-066-543-1137 | Sequence 1137, App |
| 38 | 70.4 | 13.6 | 579 | 9 | US-10-066-543-1094 | Sequence 1094, Ap |
| 39 | 70.4 | 13.6 | 586 | 9 | US-10-066-543-808 | Sequence 808, App |
| 40 | 70.4 | 13.6 | 1386 | 9 | US-10-081-119-37 | Sequence 144, App |
| 41 | 70.4 | 13.6 | 1386 | 9 | US-10-097-340-144 | Sequence 144, App |
| 42 | 70.4 | 13.6 | 1386 | 10 | US-09-962-436-283 | Sequence 293, App |
| 43 | 70.4 | 13.6 | 1356 | 10 | US-09-954-456-284 | Sequence 294, App |
| 44 | 70.4 | 13.6 | 1356 | 10 | US-09-880-107-2092 | Sequence 2092, Ap |
| 45 | 70.4 | 13.6 | 4350 | 9 | US-10-125-181-37 | Sequence 37, Appl |

ALIGNMENTS

RESULT 1
US-09-852-261-1
: Sequence 1, Application US/09852261
: Patient No. US2002008347781
: GENERAL INFORMATION:
: APPLICANT: GIDSEPIK, GEOFREY
: APPLICANT: TERENCEH, GIORGIO
: TITLE OF INVENTION: REPAIR OF NERVE DAMAGE
: FILE REFERENCE: 117-351
: CURRENT APPLICATION NUMBER: US/09/852, 261
: CURRENT FILING DATE: 2001-05-10
: PRIOR APPLICATION NUMBER: GB 0011278. 9
: PRIOR FILING DATE: 2000-05-10
: NUMBER OF SEQ ID NOS: 14
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 1
: LENGTH: 517
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-852-261-1

| | | | | |
|-----------------------|-----------------|--|-----------|-------------|
| Query Match | 100.0% | Score 517; | DB 10; | Length 517; |
| Best Local Similarity | 100.0% | Pred. No. 1.2e+159; | | |
| Matches 517; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0; |
| DB | 1 | GGACCGAGAGCGCTGCGGGGCTGAGCTGAGTGCCTTCAGTTCGTGTGGAGAC | 60 | |
| DB | 1 | GGACCGAGAGCGCTGCGGGGCTGAGCTGAGTGCCTTCAGTTCGTGTGGAGAC | 60 | |
| QY | 61 | AGGGGCTTTTATTTACACAGCCACAGGATAGTGCCTCAGAGTGGAGGCGCTCAG | 120 | |
| DB | 61 | AGGGGCTTTTATTTACACAGCCACAGGATAGTGCCTCAGAGTGGAGGCGCTCAG | 120 | |
| QY | 121 | ACAGGATGCTGATAGTGCCTTCAGAGTGCCTCAGAGTGCCTCAGAGTGCCTCAG | 180 | |
| DB | 121 | ACAGGATGCTGATAGTGCCTTCAGAGTGCCTCAGAGTGCCTCAGAGTGCCTCAG | 180 | |
| QY | 181 | TGGCAGCCCTCAGAGCTGCAGTGCCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG | 240 | |
| DB | 181 | TGGCAGCCCTCAGAGCTGCAGTGCCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG | 240 | |
| QY | 241 | ATGCCCAAGACCCAGAGTATCAGCCCATCTACCAACAGACAGAGTCTCAGAGA | 300 | |

Db 241 ATCCCAAGACCCAGAGATATACGCCCATCTACCAACAACAACAGCTCTAGACA 300
QY 301 AGGAAGAAGATACATTGTAAGAACACAGTAGAGGAGTGCAGGAACAAGACTACAG 360
Db 301 AGGAAGAAGATACATTGTAAGAACACAGTAGAGGAGTGCAGGAACAAGACTACAG 360
QY 361 GATGTAGAGACCCCTCTGAGAGTGAAGAAAGACAGCGCCAGGACCCCTTGCTCT 420
Db 361 GATGTAGAGACCCCTCTGAGAGTGAAGAAAGACAGCGCCAGGACCCCTTGCTCT 420
QY 421 GCACAGTACCTGTAACATTTGGAATACCGGCCAATAAATAGTTGATCATTTCAAA 480
Db 421 GCACAGTACCTGTAACATTTGGAATACCGGCCAATAAATAGTTGATCATTTCAAA 480
QY 481 GATGCAATTTCCCAATGAATACAGAGTAACAT 517
Db 481 GATGCAATTTCCCAATGAATACAGAGTAACAT 517

RESULT 2

US-09-852-261-5
Sequence 5, Application US/09852261
Patent No. US20020083477A1
GENERAL INFORMATION:
APPLICANT: GOLDSPIRK, GEOFFREY
APPLICANT: TERENCE, GIORGIO
TITLE OF INVENTION: REPAIR OF NERVE DAMAGE
FILE REFERENCE: 117-351
CURRENT APPLICATION NUMBER: US/09/852,261
CURRENT FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: GB 0011278.9
PRIOR FILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 5
LENGTH: 523
TYPE: DNA
ORGANISM: Oryctolagus cuniculus
US-09-852-261-5

Query Match 90.4%; Score 467.4; DB 10; Length 523;
Best Local Similarity 96.2%; Pred. No. 2,5e-143;
Matches 501; Conservative 0; Mismatches 16; Indels 4; Gaps 2;

QY 1 GGAACGGAGAGAGCTGTCGGGGGCTGAGCTGTGTGATGCTCTTCACTTCTGTGTGAGAC 60
Db 1 GGAACGGAGAGAGCTGTCGGGGGCTGAGCTGTGTGATGCTCTTCACTTCTGTGTGAGAC 60
QY 61 AGGGGCTTTATTTCAACAAGCCCAAGGATGAGCTCCAGCAGTGGAGGGGCGCTCAG 120
Db 61 AGGGGCTTTATTTCAACAAGCCCAAGGATGAGCTCCAGCAGTGGAGGGGCGCTCAG 120
QY 121 ACAAGCATCGTGTAGTGTCTCTCCGAGCTGTGTATTAAGAGGCTGAGATGTAT 180
Db 121 ACAAGCATCGTGTAGTGTCTCTCCGAGCTGTGTATTAAGAGGCTGAGATGTAT 180
QY 181 TGCCACCCCTCAAGCTCTGCAAGTCACTGCTCTGCTGCTGCCAGCGCCACACCGAG 240
Db 181 TGCCACCCCTCAAGCTCTGCAAGTCACTGCTCTGCTGCTGCCAGCGCCACACCGAG 240
QY 241 ATGCCCAAGACCCAGAGATATCAGCCCATCTACCAACAAGAACAAGAGTCTCA---G 297
Db 241 ATGCCCAAGACCCAGAGATATCAGCCCATCTACCAACAAGAACAAGAGTCTCA---G 297
QY 298 AGAAGGAAGGAATATTTGAAGAACACAAGTAGAGGAGTGCAGGAAACAAGACTA 357
Db 301 AGAAGGAAGGAATATTTGAAGAACACAAGTAGAGGAGTGCAGGAAACAAGACTA 360
QY 358 CAGAGATGTA--GAAGACCTCTGTGAGAGTGAAGAGACAGGCCACGCGAGACCCCTTG 416
Db 361 CAGAGATGTA--GAAGACCTCTGTGAGAGTGAAGAGACAGGCCACGCGAGACCCCTTG 420

QY 417 CTCGACAGTCTACCTGTAACATTTGGAATACCGGCCAATAAATAGTTGATCATTTC 476
Db 421 CTCGACAGTCTACCTGTAACATTTGGAATACCGGCCAATAAATAGTTGATCATTTC 480
QY 477 CAAGATGGCATTTTCCCAATGAATACACAAGTAACAT 517
Db 481 CAAGATGGCATTTTCCCAATGAATACACAAGTAACAT 521

RESULT 3

US-09-852-261-13
Sequence 13, Application US/09852261
Patent No. US20020083477A1
GENERAL INFORMATION:
APPLICANT: GOLDSPIRK, GEOFFREY
APPLICANT: TERENCE, GIORGIO
TITLE OF INVENTION: REPAIR OF NERVE DAMAGE
FILE REFERENCE: 117-351
CURRENT APPLICATION NUMBER: US/09/852,261
CURRENT FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: GB 0011278.9
PRIOR FILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 13
LENGTH: 471
TYPE: DNA
ORGANISM: Oryctolagus cuniculus
US-09-852-261-13

Query Match 73.0%; Score 377.2; DB 10; Length 471;
Best Local Similarity 87.8%; Pred. No. 1e-113;
Matches 455; Conservative 0; Mismatches 13; Indels 50; Gaps 2;

QY 1 GGAACGGAGAGAGCTGTCGGGGGCTGAGCTGTGTGATGCTCTTCACTTCTGTGTGAGAC 60
Db 1 GGAACGGAGAGAGCTGTCGGGGGCTGAGCTGTGTGATGCTCTTCACTTCTGTGTGAGAC 60
QY 61 AGGGGCTTTATTTCAACAAGCCCAAGGATGAGCTCCAGCAGTGGAGGGGCGCTCAG 120
Db 61 AGGGGCTTTATTTCAACAAGCCCAAGGATGAGCTCCAGCAGTGGAGGGGCGCTCAG 120
QY 121 ACAAGCATCGTGTAGTGTCTCTCCGAGCTGTGTATTAAGAGGCTGAGATGTAT 180
Db 121 ACAAGCATCGTGTAGTGTCTCTCCGAGCTGTGTATTAAGAGGCTGAGATGTAT 180
QY 181 TGCCACCCCTCAAGCTCTGCAAGTCACTGCTCTGCTGCTGCCAGCGCCACACCGAG 240
Db 181 TGCCACCCCTCAAGCTCTGCAAGTCACTGCTCTGCTGCTGCCAGCGCCACACCGAG 240
QY 241 ATGCCCAAGACCCAGAGATATCAGCCCATCTACCAACAAGAACAAGAGTCTCAGAGA 300
Db 241 ATGCCCAAGACCCAGAGATATCAGCCCATCTACCAACAAGAACAAGAGTCTCAGAGA 300
QY 301 AGGAAGAAGATACATTGTAAGAACACAAGTAGAGGAGTGCAGGAACAAGACTACAG 360
Db 256 ---AAGGAAGATACATTGTAAGAACACAAGTAGAGGAGTGCAGGAACAAGACTACAG 311
QY 361 GATGTA--GAAGACCTCTGAGAGTGAAGAAAGACAGCGCCAGGACCCCTTGCTC 419
Db 312 GATGTA--GAAGACCTCTGAGAGTGAAGAAAGACAGCGCCAGGACCCCTTGCTC 371
QY 420 TGCACAGTCTACCTGTAACATTTGGAATACCGGCCAATAAATAGTTGATCATTTCAA 479
Db 372 TGCACAGTCTACCTGTAACATTTGGAATACCGGCCAATAAATAGTTGATCATTTCAA 431
QY 480 AGATGGCATTTTCCCAATGAATACACAAGTAACAT 517
Db 432 AGATGGCATTTTCCCAATGAATACACAAGTAACAT 469

RESULT 4

US-10-136-639-4

Sequence 4, Application US/10136639
Publication No. US20030072761A1
GENERAL INFORMATION:
APPLICANT: Lebowitz, Jonathan
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TARGETING PROTEINS ACROSS THE BLOOD
FILE REFERENCE: SYM-008
CURRENT APPLICATION NUMBER: US/10/136,639
CURRENT FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: US 60/329,650
PRIOR FILING DATE: 2001-10-16
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 7260
TYPE: DNA
ORGANISM: Homo sapiens
US-10-136-639-4

Query Match
Best Local Similarity 87.3%; Pred. No. 2,8e-102;
Matches 455; Conservative 0; Mismatches 13; Indels 53; Gaps 5;

QY 1 GGACCGGAGAGCGCTCTGGGGGCTGAGCTGTGATGCTCTTCAAGTTGTTGGAGAC 60
DB 311 GGACCGGAGAGCGCTCTGGGGGCTGAGCTGTGATGCTCTTCAAGTTGTTGGAGAC 370
QY 61 AGGGGCTTTTATTATTAACAAGCCCAAGGATATGCTCCACAGTCGAGAGGCGCTCAG 120
DB 371 AGGGGCTTTTATTATTAACAAGCCCAAGGATATGCTCCACAGTCGAGAGGCGCTCAG 430
QY 121 ACAGGCATCTGGATGATGATGCTGCTCCGAGCTGTATCTAAGAGGCTGAGATGTAT 180
DB 431 ACAGGCATCTGGATGATGATGCTGCTCCGAGCTGTATCTAAGAGGCTGAGATGTAT 490
QY 181 TGGCGACCCCTTCAAGCCCTGCGCAAGTCAGCTGCTGTGCTGCGCCAGCCACACCGAC 240
DB 491 TGGCGACCCCTTCAAGCCCTGCGCAAGTCAGCTGCTGTGCTGCGCCAGCCACACCGAC 550
QY 241 ATGCCCAAGACCCCAAGATATCAGCCCATCTACCAACAAGAACAGTCTCAGAGA 300
DB 551 ATGCCCAAGACCCCAAGATATCAGCCCATCTACCAACAAGAACAGTCTCAGAGA 565
QY 301 AGGAAGAGAGTACATTTGAAGACACAGTATGAGAGGAGTGCAGGAAACAGAACTACAG 360
DB 566 ---AAGGAAGTACATTTGAAGACACAGTATGAGAGGAGTGCAGGAAACAGAACTACAG 621
QY 361 GATGTA-GAAGACCTTCTGAGAGTGAAGAAGACAGCCAGCCAGACCTTTGCTC 419
DB 622 GATGTAAGAGAGACCTTCTGAGAGTGAAGAAGTGAAGTGAATGCCAGCCAGAGATCCTTTGCTC 681
QY 420 TGCAC-AGTTACCTG-TAAACATTGGAATPACCGGCAAAAATAAGTTGATCATTTC 477
DB 682 TGCACAGAGTTACCTGTTAACTTTGGAACACCTACCAAAAATAAGTTGATCATTTC 741
QY 478 AAGAT-GGCAATTTCCCAATGAATACACAGTAAACAT 517
DB 742 AAGATGGGCGTTTCCCAATGAATACACAGTAAACAT 782

RESULT 5
US-09-919-497-24
Sequence 24, Application US/09919497
Patent No. US2002010662A1
GENERAL INFORMATION:
APPLICANT: Mutter, George L.
TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
FILE REFERENCE: B0801/725
CURRENT APPLICATION NUMBER: US/09/919,497
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/221,735
PRIOR FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 100

SOFTWARE: PatentIn version 3.0
SEQ ID NO 24
LENGTH: 7260
TYPE: DNA
ORGANISM: Homo sapiens
US-09-919-497-24

Query Match
Best Local Similarity 87.3%; Pred. No. 2,8e-102;
Matches 455; Conservative 0; Mismatches 13; Indels 53; Gaps 5;

QY 1 GGACCGGAGAGCGCTCTGGGGGCTGAGCTGTGATGCTCTTCAAGTTGTTGGAGAC 60
DB 311 GGACCGGAGAGCGCTCTGGGGGCTGAGCTGTGATGCTCTTCAAGTTGTTGGAGAC 370
QY 61 AGGGGCTTTTATTATTAACAAGCCCAAGGATATGCTCCACAGTCGAGAGGCGCTCAG 120
DB 371 AGGGGCTTTTATTATTAACAAGCCCAAGGATATGCTCCACAGTCGAGAGGCGCTCAG 430
QY 121 ACAGGCATCTGGATGATGATGCTGCTCCGAGCTGTATCTAAGAGGCTGAGATGTAT 180
DB 431 ACAGGCATCTGGATGATGATGCTGCTCCGAGCTGTATCTAAGAGGCTGAGATGTAT 490
QY 181 TGGCGACCCCTTCAAGCCCTGCGCAAGTCAGCTGCTGTGCTGCGCCAGCCACACCGAC 240
DB 491 TGGCGACCCCTTCAAGCCCTGCGCAAGTCAGCTGCTGTGCTGCGCCAGCCACACCGAC 550
QY 241 ATGCCCAAGACCCCAAGATATCAGCCCATCTACCAACAAGAACAGTCTCAGAGA 300
DB 551 ATGCCCAAGACCCCAAGATATCAGCCCATCTACCAACAAGAACAGTCTCAGAGA 565
QY 301 AGGAAGAGAGTACATTTGAAGACACAGTATGAGAGGAGTGCAGGAAACAGAACTACAG 360
DB 566 ---AAGGAAGTACATTTGAAGACACAGTATGAGAGGAGTGCAGGAAACAGAACTACAG 621
QY 361 GATGTA-GAAGACCTTCTGAGAGTGAAGAAGACAGCCAGCCAGACCTTTGCTC 419
DB 622 GATGTAAGAGAGACCTTCTGAGAGTGAAGAAGTGAAGTGAATGCCAGCCAGAGATCCTTTGCTC 681
QY 420 TGCAC-AGTTACCTG-TAAACATTGGAATPACCGGCAAAAATAAGTTGATCATTTC 477
DB 682 TGCACAGAGTTACCTGTTAACTTTGGAACACCTACCAAAAATAAGTTGATCATTTC 741
QY 478 AAGAT-GGCAATTTCCCAATGAATACACAGTAAACAT 517
DB 742 AAGATGGGCGTTTCCCAATGAATACACAGTAAACAT 782

RESULT 6
US-09-880-107-3739
Sequence 3739, Application US/09880107
Patent No. US20020142981A1
GENERAL INFORMATION:
APPLICANT: Horne, Darci T.
APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Uwe
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REFERENCE: 44921-3028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3739
LENGTH: 7260
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Genbank Accession No. US20020142981A1 X57025


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Db 319 TGTGCCCCACTGAACTCTACAAAGCAGCCCGCTTATTCGTCGTCACCGCCACGACCTGAC 378
Qy 241 ATGCCCAAGACCCAGATATCAGCCCGCATCTACCAACAAGAACGAGTCTCA---G 297
Db 379 ATGCCCAAGACCTCAAGATCCCGCTCTATGACAAACAAGAACGAGTCTCAAGG 438
Qy 298 AGAAGGAAGAGATGATTTGAACAACAGTGAAGAGAGTGAAGAGAGTGAAGAGAGTGAAG 357
Db 439 AGAAGGAAGAGATGATTTGAACAACAGTGAAGAGAGTGAAGAGAGTGAAGAGAGTGAAG 498
Qy 358 CAGATATGA-GAAGACCCCTTGTGAAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 416
Db 499 CAGATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 558
Qy 417 CTCTGACAGATTAAGTCTGTAAGATGGAATACCGGCA-----AAAAATGATTTGATC 470
Db 559 CTGCTTGAGCAACCTGCAAAACATGAAACACCTTACCAATATACATATATATGTCATTA 618
Qy 471 ACATTTCAAGAT-GGCATTTTCCCAATGAAA 502
Db 619 ACATTTCAAGATGGGCAATTTCCCAATGAAA 651
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RESULT 9
US-09-852-261-9
; Sequence 9, Application US/09852261
; Patent No. US20020083477A1
; GENERAL INFORMATION:
; APPLICANT: TERENGI, GIORGIO
; APPLICANT: GOLDSPIK, GIORGIO
; TITLE OF INVENTION: REPAIR OF NERVE DAMAGE
; FILE REFERENCE: 117-351
; CURRENT APPLICATION NUMBER: US/09/852,261
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: GB 0011278.9
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO: 9
; LENGTH: 318
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-852-261-9
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Query Match 50.0%; Score 258.4; DB 10; Length 318;
Best Local Similarity 99.6%; Pred. No. 9, 5e-75;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGACCGGAGAGCTCTGCGGGGCTGAGCTGTGATGCTCTTCACTTGTGTGTGAGAG 60
Db 1 GGACCGGAGAGCTCTGCGGGGCTGAGCTGTGATGCTCTTCACTTGTGTGTGAGAG 60
Qy 61 AGGGGCTTTTATTTCAACAAGCCACAGGATATGCTCCAGAGTGGAGGCGGCTCAG 120
Db 61 AGGGGCTTTTATTTCAACAAGCCACAGGATATGCTCCAGAGTGGAGGCGGCTCAG 120
Qy 121 AAGAGCATGCTGATGAGTGTCTTCCGAGCTGTATCTAAGAGAGCTGAGATGTAT 180
Db 121 AAGAGCATGCTGATGAGTGTCTTCCGAGCTGTATCTAAGAGAGCTGAGATGTAT 180
Qy 181 TGCAGACCCCTCAAGCTGCGAGTCACTGCTGTCCGTGCCAGCGCCACCGCAG 240
Db 181 TGCAGACCCCTCAAGCTGCGAGTCACTGCTGTCCGTGCCAGCGCCACCGCAG 240
Qy 241 ATGCCCAAGACCCAGATGA 260
Db 241 ATGCCCAAGACCCAGATGA 260
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RESULT 10
US-09-852-261-11
; Sequence 11, Application US/09852261
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; Patent No. US20020083477A1
; GENERAL INFORMATION:
; APPLICANT: GOLDSPIK, GIORGIO
; APPLICANT: TERENGI, GIORGIO
; TITLE OF INVENTION: REPAIR OF NERVE DAMAGE
; FILE REFERENCE: 117-351
; CURRENT APPLICATION NUMBER: US/09/852,261
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: GB 0011278.9
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO: 11
; LENGTH: 487
; TYPE: DNA
; ORGANISM: Rattus sp.
US-09-852-261-11
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Query Match 47.9%; Score 247.8; DB 10; Length 487;
Best Local Similarity 74.5%; Pred. No. 3, 6e-71;
Matches 391; Conservative 0; Mismatches 77; Indels 57; Gaps 4;

Qy 1 GGACCGGAGAGCTCTGCGGGGCTGAGCTGTGATGCTCTTCACTTGTGTGAGAG 60
Db 1 GGACCGGAGAGCTCTGCGGGGCTGAGCTGTGATGCTCTTCACTTGTGTGAGAG 60
Qy 61 AGGGGCTTTTATTTCAACAAGCCACAGGATATGCTCCAGAGTGGAGGCGGCTCAG 120
Db 61 AGGGGCTTTTATTTCAACAAGCCACAGGATATGCTCCAGAGTGGAGGCGGCTCAG 120
Qy 121 ACAGCATCTGATGAGTGTCTTCCGAGCTGTATCTAAGAGAGCTGAGATGTAT 180
Db 121 ACAGCATCTGATGAGTGTCTTCCGAGCTGTATCTAAGAGAGCTGAGATGTAT 180
Qy 181 TGCAGACCCCTCAAGCTGCGAGTCACTGCTGTCCGTGCCAGCGCCACCGCAG 240
Db 181 TGCAGACCCCTCAAGCTGCGAGTCACTGCTGTCCGTGCCAGCGCCACCGCAG 240
Qy 241 ATGCCCAAGACCCAGATGA 260
Db 241 ATGCCCAAGACCCAGATGA 260
Qy 301 AGAAGAGATGATTTGAAGAACACAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 360
Db 256 ---AAGAGATGATTTGAAGAACACAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 311
Qy 361 GATGTA-GAAGACCCCTTCTGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 419
Db 312 AATGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 371
Qy 420 TGCAAGTACCTTAAACATTTGAATACCGGCA-----AAAAATGATTTGATCACA 473
Db 372 CTGAGAGAGCTGCAAAACATGGAACACCTGCAAAATATCAATATGATGATCA 431
Qy 474 TTTCAAAGAT-GGCATTTTCCCAATGAATATACAGATTAAGAT 517
Db 432 TTTCAGAGATGGGATTTTCCCTCAATGATATACAGATTAAGAT 476
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RESULT 11
US-10-238-114-1
; Sequence 1, Application US/10238114
; Publication No. US20030100073A1
; GENERAL INFORMATION:
; APPLICANT: Meriel
; APPLICANT: ANDREONI, Christine Michele
; TITLE OF INVENTION: IGF-1 AS FELINE VACCINE ADJUVANT, IN PARTICULAR AGAINST FELINE
; FILE REFERENCE: 454313-3165.1
; CURRENT APPLICATION NUMBER: US/10/238,114
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: FR 01 11736
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/318,666
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PRIOR FILING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 462
TYPE: DNA
ORGANISM: Felis catus
US-10-238-114-1

Query Match 44.1%; Score 228; DB 9; Length 462;
Best Local Similarity 92.3%; Pred. No. 1,1e-64;
Matches 240; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 GGACCGGAGAGCGCTCTGCGGGGCTGAGCTGGATGCTTTCAGTTCGTGTGAGAGC 60
DB 145 GGACCAAGAGAGCGCTCTGCGGGGCTGAGTGTGAGACCTTTCAGTTCGTGTGAGAGC 264
QY 61 AGGGGCTTTTATTTCAACAAGCCCAAGCGGTATGCTCCAGCAGTCCGAGCGCCCTCAG 120
DB 205 AGGGGCTTTTATTTCAACAAGCCCAAGCGGTATGCTCCAGCAGTCCGAGCGCCCTCAG 264
QY 121 ACAGGATCGTGATGATGCTGCTTCCGAGCTGTATGATTAAGGAGGCTGAGATGTAT 180
DB 265 ACAGGATCGTGATGATGCTGCTTCCGAGCTGTATGATTAAGGAGGCTGAGATGTAT 324
QY 181 TGGCGACCCCTCAAGCCTGCGCAAGTCACTGCTGCTCCGTCGCCAGCCGACACCGAC 240
DB 325 TGTGACCCCTCAAGCCTGCGCAAGTCACTGCTGCTCCGTCGCCAGCCGACACCGAC 384
QY 241 ATGCCCAAGACCCAGAGTA 260
DB 385 ATGCCCAAGGCTCAGAAAGA 404

RESULT 12

US-09-930-377B-1

Sequence 1, Application US/09930377B
Patent No. US20020144296A1

GENERAL INFORMATION:
APPLICANT: Wheeler, Matthew B.
APPLICANT: Donovan, Sharon M.
APPLICANT: Bleck, Gregory T.
APPLICANT: Monaco-Seigel, Marcia
TITLE OF INVENTION: Animals Expressing Exogenous IGF-I in their Milk
FILE REFERENCE: 66-00
CURRENT APPLICATION NUMBER: US/09/930,377B
CURRENT FILING DATE: 2001-08-15
PRIOR APPLICATION NUMBER: 60/225,474
PRIOR FILING DATE: 2000-08-15
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 4532
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: alpha-1A/IGF-I
US-09-930-377B-1

Query Match 39.6%; Score 204.6; DB 10; Length 4532;
Best Local Similarity 95.9%; Pred. No. 1,7e-56;
Matches 210; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 GGACCGGAGAGCGCTCTGCGGGGCTGAGCTGGATGCTTTCAGTTCGTGTGAGAGC 60
DB 2046 GGACCGGAGAGCGCTCTGCGGGGCTGAGCTGGATGCTTTCAGTTCGTGTGAGAGC 2105
QY 61 AGGGGCTTTTATTTCAACAAGCCCAAGCGGTATGCTCCAGCAGTCCGAGCGCCCTCAG 120
DB 2106 AGGGGCTTTTATTTCAACAAGCCCAAGCGGTATGCTCCAGCAGTCCGAGCGCCCTCAG 2165
QY 121 ACAGGATCGTGATGATGCTGCTTCCGAGCTGTATGATTAAGGAGGCTGAGATGTAT 180

DB 2166 ACAGGATCGTGATGATGCTGCTTCCGAGCTGTATCTTAAGAGGCTGAGATGTAT 2225
QY 181 TGGCGACCCCTCAAGCCTGCGCAAGTCACTGCTGCTGTC 219
DB 2226 TGGCGACCCCTCAAGCCTGCGCAAGTCACTGCTGATGATGCTC 2264

RESULT 13

US-09-930-377B-2

Sequence 2, Application US/09930377B
Patent No. US20020144296A1

GENERAL INFORMATION:
APPLICANT: Wheeler, Matthew B.
APPLICANT: Donovan, Sharon M.
APPLICANT: Bleck, Gregory T.
APPLICANT: Monaco-Seigel, Marcia
TITLE OF INVENTION: Animals Expressing Exogenous IGF-I in their Milk
FILE REFERENCE: 66-00
CURRENT APPLICATION NUMBER: US/09/930,377B
CURRENT FILING DATE: 2001-08-15
PRIOR APPLICATION NUMBER: 60/225,474
PRIOR FILING DATE: 2000-08-15
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 210
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: IGF-I
US-09-930-377B-2

Query Match 39.4%; Score 203.6; DB 10; Length 210;
Best Local Similarity 98.1%; Pred. No. 8e-57;
Matches 206; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGACCGGAGAGCGCTCTGCGGGGCTGAGCTGGATGCTTTCAGTTCGTGTGAGAGC 60
DB 1 GGACCGGAGAGCGCTCTGCGGGGCTGAGCTGGATGCTTTCAGTTCGTGTGAGAGC 60
QY 61 AGGGGCTTTTATTTAAACAAGCCCAAGGATATGCTCCAGAGTCCGAGCGCCCTCAG 120
DB 61 AGGGGCTTTTATTTAAACAAGCCCAAGGATATGCTCCAGAGTCCGAGCGCCCTCAG 120
QY 121 ACAGGATCGTGATGATGCTGCTTCCGAGCTGTATGATTAAGGAGGCTGAGATGTAT 180
DB 121 ACAGGATCGTGATGATGCTGCTTCCGAGCTGTATGATTAAGGAGGCTGAGATGTAT 180
QY 181 TGGCGACCCCTCAAGCCTGCGCAAGTCACTGCTGCT 210
DB 181 TGGCGACCCCTCAAGCCTGCGCAAGTCACTGCT 210

RESULT 14

US-10-179-046-13

Sequence 13, Application US/10179046
Publication No. US20030013154A1

GENERAL INFORMATION:
APPLICANT: Crawford, Kenneth
Zator, Isabel
Indis, Michael
TITLE OF INVENTION: Pichia Secretary Leader for Protein Expression

NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSER: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: California
COUNTRY: United States
ZIP: 94608
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/179,046
FILING DATE: 25-Jun-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/029,267
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Chung, Ling-Fong
REGISTRATION NUMBER: 36,482
REFERENCE/DOCKET NUMBER: 1165.100
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2704
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 390 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Synthetic"
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-179-046-13

Query Match 39.2%; Score 202.8; DB 9; Length 390;
Best Local Similarity 96.7%; Pred. No. 2e-56; Indels 0; Gaps 0;
Matches 207; Conservative 0; Mismatches 7;

QY 1 GGACCGGACGACCTCTGCGGGGCTGAGCTGTGATGCTTCCTTCAGTGTGTGAGAC 60
DB 160 GGACCGGACGACCTCTGCGGGGCTGAGCTGTGATGCTTCCTTCAGTGTGTGAGAC 219
QY 61 AGGGGCTTTATTTTCAACAGCCCAAGGGTATGGCTCCAGCAGTCGAGGGCGCTCAG 120
DB 220 AGGGGCTTTATTTTCAACAGCCCAAGGGTATGGCTCCAGCAGTCGAGGGCGCTCAG 279
QY 121 ACAGGATCGTGTGATGAGTGTCTTCCGAGCTGTGATCTAAGAGGCTGGAGATGTAT 180
DB 280 ACAGGATCGTGTGATGAGTGTCTTCCGAGCTGTGATCTAAGAGGCTGGAGATGTAT 339
QY 181 TGGCAGCCCTCAGGCTGCCAAGTCACTGCTGCT 214
DB 340 TGGCAGCCCTCAGGCTGCCAAGTCACTGCTGCT 373

RESULT 15

US-10-161-088-3
Sequence 3, Application US/10161088
Publication No. US2003007761A1
GENERAL INFORMATION:
APPLICANT: Parrow, Vendela
APPLICANT: Rosegren, Linda
TITLE OF INVENTION: NEW METHODS
FILE REFERENCE: 13425-111001
CURRENT APPLICATION NUMBER: US/10/161,088
CURRENT FILING DATE: 2002-05-31
PRIOR APPLICATION NUMBER: SE 0101934-8
PRIOR FILING DATE: 2001-06-01
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 286
TYPE: DNA
ORGANISM: Homo sapiens
US-10-161-088-3

Query Match 39.1%; Score 202; DB 9; Length 286;
Best Local Similarity 88.0%; Pred. No. 3.1e-56;

Matches 220; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
QY 16 TGGCGGCTGAGCTGGTGGATGCTTCCTTCAGTGTGTGTGAGACAGAGGCTTTATTTTC 75
DB 18 TGGCGGCTGAGCTGGTGGATGCTTCCTTCAGTGTGTGTGAGACAGAGGCTTTATTTTC 77
QY 76 AACAGCCCAAGGATGCTCCAGCAGTCGAGGCGGCTCAGACAGGCTATGAT 135
DB 78 AACAGCCCAAGGCTATGCTCCAGCAGTCGAGGCGGCTCAGACAGGCTATGAT 137
QY 136 GAGTGTCTTCCGAGCTGTGATCTAAGAGGCTGAGATGTATTGGCACCCTCAG 195
DB 138 GAGTGTCTTCCGAGCTGTGATCTAAGAGGCTGAGATGTATTGGCACCCTCAG 197
QY 196 CCTGCCAAGTCAGCTCGCTCGTCCGAGCCAGCCAGCCAGCATGCCAAGACCCAG 255
DB 198 CTTCAAAAGCAGCCCGCTCTATCCGTCGTCGAGCCAGCCAGCATGCCAAGACCCAG 257
QY 256 AAGTATCAGC 265
DB 258 GCATGCAAGC 267

Search completed: June 15, 2003, 20:22:23
Job time : 95.6428 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 15, 2003, 15:41:03 ; Search time 1099.81 Seconds
(without alignments)
7613.181 Million cell updates/sec

Title: US-09-852-261-1

Perfect score: 517
Sequence: 1 gacacggagacgcctctgcg.....tgaatcacacaagtaaacat 517

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_estl:*
10: gb_estl2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pin:*
21: em_gss_vit:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| C 1 | 331.6 | 64.1 | 558 | 9 | A1503976 |
| C 2 | 330.6 | 63.9 | 558 | 14 | BM984670 |
| C 3 | 329.8 | 63.8 | 558 | 10 | AM146128 |
| C 4 | 326.6 | 63.2 | 575 | 9 | A1248089 |
| C 5 | 316.6 | 61.2 | 549 | 9 | A1169253 |
| C 6 | 315.8 | 61.1 | 558 | 9 | A1265629 |

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|------|-------|------|-----|----|----------|
| C 7 | 314.8 | 60.9 | 498 | 9 | AA542914 |
| C 8 | 309 | 59.8 | 816 | 9 | A1118218 |
| C 9 | 303.6 | 58.7 | 594 | 12 | BF383724 |
| C 10 | 299.8 | 58.0 | 527 | 9 | AA913900 |
| C 11 | 289.6 | 56.0 | 642 | 9 | A1876493 |
| C 12 | 287.4 | 55.6 | 499 | 10 | AM495481 |
| C 13 | 276 | 53.4 | 468 | 9 | A1169770 |
| C 14 | 274.4 | 53.1 | 882 | 9 | A1604642 |
| C 15 | 268.2 | 51.9 | 430 | 9 | A1478804 |
| C 16 | 268.2 | 50.9 | 653 | 14 | BQ200567 |
| C 17 | 258.4 | 50.0 | 608 | 9 | AL599807 |
| C 18 | 254.6 | 49.2 | 486 | 9 | AA936559 |
| C 19 | 254.2 | 49.2 | 521 | 10 | AM493459 |
| C 20 | 254.2 | 49.2 | 559 | 13 | B1715603 |
| C 21 | 254.2 | 49.2 | 621 | 13 | B1221656 |
| C 22 | 254 | 49.1 | 356 | 10 | AM297586 |
| C 23 | 253.2 | 49.0 | 595 | 9 | A1573421 |
| C 24 | 252.6 | 48.9 | 499 | 13 | B1676839 |
| C 25 | 252.6 | 48.9 | 500 | 9 | AA945553 |
| C 26 | 252.6 | 48.9 | 525 | 9 | AA963258 |
| C 27 | 251.4 | 48.6 | 482 | 9 | AA456717 |
| C 28 | 251 | 48.5 | 706 | 9 | A1401719 |
| C 29 | 249.4 | 48.2 | 525 | 9 | A1598751 |
| C 30 | 248.6 | 48.1 | 665 | 9 | AA690767 |
| C 31 | 247.8 | 47.9 | 559 | 13 | B1715465 |
| C 32 | 247.4 | 47.9 | 799 | 9 | A1314558 |
| C 33 | 247.2 | 47.8 | 499 | 13 | B1294072 |
| C 34 | 244.2 | 47.2 | 502 | 9 | A1104659 |
| C 35 | 243 | 47.0 | 561 | 13 | B1714874 |
| C 36 | 240.6 | 46.5 | 564 | 13 | B1714981 |
| C 37 | 237.4 | 45.9 | 588 | 13 | B1715475 |
| C 38 | 237.2 | 45.9 | 480 | 9 | AA621551 |
| C 39 | 236.8 | 45.8 | 512 | 9 | A1876203 |
| C 40 | 233.8 | 45.0 | 637 | 10 | AM413016 |
| C 41 | 233.6 | 45.0 | 779 | 9 | AA867155 |
| C 42 | 231 | 44.7 | 473 | 9 | AA451360 |
| C 43 | 230.8 | 44.6 | 773 | 13 | B1445500 |
| C 44 | 230.2 | 44.5 | 475 | 9 | A1033043 |
| C 45 | 227.6 | 44.0 | 474 | 9 | A1526955 |

ALIGNMENTS

RESULT 1
A1503976/c 558 bp mRNA linear EST 11-MAR-1999
LOCUS
DEFINITION
vm33d08.xl Stratiogene mouse diaphragm (#937303) Mus musculus cDNA
clone IMAGE:1001007 3' similar to gb:X04482 Mouse mRNA for
preproinsulin-like growth factor IB (MOUSE);, mRNA sequence.

ACCESSION
A1503976
VERSION
A1503976.1 GI:4401827
KEYWORDS
EST.

ORGANISM
Mus musculus
house mouse.

REFERENCE
AUTHORS
Marrin,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person
B., Swaller,T., Gibbons,M., Page,D., Harvey,N., Schurk,R., Ritter
E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
Waterston,R. and Wilson,R.
The WashU-NCI Mouse EST Project 1999

TITLE
JOURNAL
COMMENT
Unpublished (1999)
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu

This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

MC1:565223
This clone was previously sequenced on the 5' end only, this new data is from the 3' end
High quality sequence step: 440.
Location/Qualifiers
1...558
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:1001007"
/issue="Stratagene mouse diaphragm (#937303)"
/dev_stage="adult"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: diaphragm; Vector: pBluescript SK-; Site: 1; prepared from diaphragm muscle. Primer: oligo dT. Average insert size: 1.5 kb. Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGACGAG 3' -3' adaptor sequence: 5' CTCGAGTTTCTTTTCTTTT 3'."

BASE COUNT 103 a 133 c 149 g 173 t
ORIGIN

Query Match 64.1%; Score 331.6; DB 9; Length 558;
Best Local Similarity 82.0%; Pred. No. 1,4e-87;
Matches 433; Conservative 0; Mismatches 84; Indels 11; Gaps 4;

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QY 1 GGACCGGAGACGCTCTGCGGGCTGAGCTGATGCTCTTCAGTCTGTGTGGAGAC 60
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Db 530 GGACCGGAGACGCTCTGCGGGCTGAGCTGATGCTCTTCAGTCTGTGTGGAGAC 471
QY 61 AGGGGCTTTATTTCAACAAGCCACAGGTATGCTCCAGCAGTGGAGGGCGCTCAG 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 470 AGGGGCTTTATTTCAACAAGCCACAGGTATGCTCCAGCAGTGGAGGGCGCTCAG 411
QY 121 ACAAGCATCTGTGATGCTGCTCTCCGAGCTGTGATCTAGAGAGCTGAGATGTAT 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 410 ACAAGCATCTGTGATGCTGCTCTCCGAGCTGTGATCTAGAGAGCTGAGATGTAT 351
QY 181 TGGCACCCTCAAGCTCCGACAGTCACTGCTCTGCTCCGACCGCCACACCGAC 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 350 TGTGCCCCACTGAGAGCTACAAAAGCCGCCGCTCTATCCGTCGCCACCGCCACTGTAC 291
QY 241 ATGCCCAAGACCCGAGAGTATCAGCCCATCTACCAACAAGACGAGAGTCTCA---G 297
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 290 ATGCCCAAGACTGAGAGTCCCGCTCCCTATTCGACAAACAAGAAAGAGTCTCAAG 231
QY 298 AGAAGGAAGAGTACATTGAGAAACACAGTGAAGAGTGCAGGAAACAAGACTA 357
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 230 AGAAGGAAGAGTACATTGAGAAACACAGTGAAGAGTGCAGGAAACAAGACTA 171
QY 358 CAGAGATGA-GAAGACCTCTCTGAGAGTGAAGAGACAGGACCGGAGACCCCTTG 416
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 170 CAGAGATGAAGAGAGTCTCCCGACGAGCAGAAATGCCATACCGCGAGATCTCTTG 111
QY 417 CTCTGCACTTACCTCTTAACATTTGGAATATCGCGCCA-----AAATATAGTTGATC 470
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 110 CTCTGCACTTACCTCTTAACATTTGGAATATCGCGCCA-----AAATATAGTTGATC 51
QY 471 ACATTGAAGAT-GGCACTTCCCGCAATGAATATACCAAGTAAACAT 517
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Db 50 ACATTGAAGATGGCACTTCCCGCAATGAATATACCAAGTAAACAT 3
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RESULT 2
BM984670/c 673 bp mRNA linear EST 21-MAR-2002
LOCUS BM984670
DEFINITION UT-CF-ECL-abj-k-24-0-UI-s1 UT-CF-ECL Homo sapiens cDNA clone
ACCESSION BM984670
VERSION BM984670.1 GI:19610417
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
COMMENT
McCrackay Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul.mccrackay@uiowa.edu
Tissue procurement: Dr. M. J. Welsh, University of Iowa
cDNA library preparation: Dr. M. Bento Soares, University of Iowa
cDNA library arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
-Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).
Seq primer: M13 FORWARD
PolyA-Tes.

FEATURES
source
Location/Qualifiers
1...673
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="UI-CF-ECL-abj-k-24-0-UI"
/clone_lib="UI-CF-ECL"
/issue="Lung"
/dev_stage="Adult and Fetal"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/note="Organ: Lung; Vector: p773-Pac (Pharmacia) with a modified polylinker; Site: 1; Ecor I; Site: 2; Not I; UI-CF-ECL is a normalized cDNA library containing the following tissue(s): Normal lung from adult and from fetal day 64, day 87, week 19 and week 42. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an Ecor I adaptor, digested with Not I, and cloned directionally into p773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AGTGCCTTAC.
TAG_LIB=UI-CF-ECL
TAG_TISSUE=Normal Lung Epithelial Cells Tissue nos 369-371 and 380-383
TAG_SEQ=AGTGCCTTAC"

BASE COUNT 152 a 164 c 169 g 188 t
ORIGIN

Query Match 63.9%; Score 330.6; DB 14; Length 673;
Best Local Similarity 86.9%; Pred. No. 2.9e-87;
Matches 453; Conservative 0; Mismatches 14; Indels 54; Gaps 6;

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QY 1 GGACCGGAGACGCTCTGCGGGCTGAGCTGATGCTCTTCAGTCTGTGTGGAGAC 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 492 GGACCGGAGACGCTCTGCGGGCTGAGCTGATGCTCTTCAGTCTGTGTGGAGAC 433
QY 61 AGGGGCTTTATTTCAACAAGCCACAGGTATGCTCCAGCAGTGGAGGGCGCTCAG 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 432 AGGGG-TTTATTTCAACAAGCCACAGGTATGCTCCAGCAGTGGAGGGCGCTCAG 374
QY 121 ACAAGCATCTGTGATGCTGCTCTCCGAGCTGTGATCTAGAGAGCTGAGATGTAT 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 373 ACAAGCATCTGTGATGATGCTCTCCGAGCTGTGATCTAGAGAGCTGAGATGTAT 314
QY 181 TGGCACCCTCAAGCTCCGACAGTCACTGCTCTGTCCGACCGCCACACCGAC 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 313 TGGCACCCTCAAGCTCCGACAGTCACTGCTCTGTCCGACCGCCACACCGAC 254
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QY 241 ATGCCAAGACCCAGATATCAGGCCCCCTCTACCAACAGAACAGCAAGTCTCAGGA 300
 Db 253 ATGCCAAGACCCAG----- 239
 QY 301 AGGAAGAAGAGTACATTTGAAGAACAGTAGAGGAGTGCAGGAACAGAACTACAG 360
 Db 238 ----AAGAGATGACATTTGAAGAACAGTAGAGGAGTGCAGGAACAGAACTACAG 183
 QY 361 GATGTA-GAAGACCTTTCTGAGAGTGAAGAGCAGCAGCCAGACCTTTGCTC 419
 Db 182 GATGTAAGAACCCCTCTGAGAGTGAAGATGACATGACCCAGACCTTTGCTC 123
 QY 420 TGCAC-AGTTACCTG-TAACAATGAAATACCGGCAAAATAATGATTGATCATCTTC 477
 Db 122 TGCACAGTACTCTGTATTAACCTTTGAGACACTACCAAAATAATGATTGATCATTTA 63
 QY 478 AAGAT-GGCATTTCCCAATGAATAACACAGTAACAT 517.
 Db 62 AAGATGGGCGTTTCCCAATGAATAACACAGTAACAT 22
 RESULT 3
 AM146128/c 623 bp mRNA linear EST 10-OCT-2000
 LOCUS um37e10.x1 Sugano mouse embryo mewa Mus musculus cDNA clone
 DEFINITION IMAGE:2247498.3' similar to gb:X04482 Mouse mRNA for
 preproinsulin-like growth factor IB (MOUSE);, mRNA sequence.
 AM146128
 ACCESSION AM146128.1 GI:6167864
 VERSION EST.
 KEYWORDS house mouse.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 623)
 REFERENCE Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, F., Person
 B., Waller, T., Gibbons, M., Pape, D., Harvey, N., Schuck, R., Rittler
 E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
 Waterson, R. and Wilson, R.
 The WashU-NCI Mouse EST Project 1999
 TITLE Unpublished (1999)
 JOURNAL Contact: Maria M/WashU-NCI Mouse EST Project 1999
 COMMENT Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1810
 Fax: 314 286 1810
 Email: mouseest@wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 MG1:1006958
 Seq primer: custom primer used
 High quality sequence stop: 499.
 Location/Qualifiers
 1. 623
 /organism="Mus musculus"
 /strain="C57BL"
 /db_xref="taxon:10090"
 /clone="IMAGE:2247498"
 /clone_lib="Sugano mouse embryo mewa"
 /dev_stage="embryo, 14 dpc"
 /lab_host="DH10B"
 /note="Vector: PME18S-FL3; site 1: DraIII (CACTGATG);
 site 2: DraIII (CAGCAGTGC); 1st strand cDNA was primed
 with an oligo(dT) primer [ATGTGGCTTTTCTTTTCTTTT];
 double-stranded cDNA was ligated to a DraIII adaptor
 [GTGGCTTACTG], digested and cloned into digested DraIII
 sites of the PME18S-FL3 vector (5' site CACTGATG, 3' site
 CAGCAGTGC). XhoI should be used to isolate the cDNA
 insert. Size selection was performed to exclude fragments
 <1.5kb. Library constructed by Dr. Sumio Sugano
 (University of Tokyo Institute of Medical Science).

BASE COUNT 123 a 138 c 170 g 191 t 1 others
 ORIGIN
 Query Match 63.8%; Score 329.8; DB 10; Length 623;
 Best Local Similarity 80.6%; Pred. No. 5e-87;
 Matches 425; Conservative 0; Mismatches 92; Indels 10; Gaps 3;
 Custom primers for sequencing: 5' end primer
 CTTCGCTTAAGAGCTGCG and 3' end primer
 CGACCTGCAGCTGAGACCA.

QY 1 GGACCGAGACGCTCTCGGGGCTGAGCTGTGATCTTTTCACTTCTGTGTGAGAC 60
 Db 541 GGACCGAGACGCTCTTCGGGGCTGAGCTGTGATCTTTTCACTTCTGTGTGAGAC 482
 QY AGGGCTTTTATTCAACAAGCCACAGGGATATGGCTCCAGAGTGGAGGGGCTCAG 120
 Db 481 AGGGCTTTTACTTCAACAAGCCACAGGGATATGGCTCCAGAGTGGAGGGGCTCAG 422
 QY 121 ACAGGCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
 Db 421 ACAGGCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 362
 QY 181 TGGCACCCTCCAGCCTGCGCAAGTCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCT 240
 Db 361 TGGCACCCTCCAGCCTGCGCAAGTCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCT 302
 QY 241 ATGCCAAGACCCAGAGTATCAAGCCCACTTCAACAAGAACAGAGAGTCTCA---G 297
 Db 301 ATGCCAAGACCTCAAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 242
 QY 298 AGAAGAAAGAGAGTATTTGAAGAACACAGTAGAGGAGTGCAGGAACAGAACTA 357
 Db 241 AGAAGAAAGAGAGTATTTGAAGAACACAGTAGAGGAGTGCAGGAACAGAACTA 182
 QY 358 CAGAGTGA-GAAGACCTCTGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 416
 Db 181 CAGAGTGAAG 122
 QY 417 CTCTGCACAGTCTGATTAACATTTGAAGAACAGAGAGAGAGAGAGAGAGAG 470
 Db 121 CTCTGCACAGTCTGATTAACATTTGAAGAACAGAGAGAGAGAGAGAGAGAG 62
 QY 471 ACATTTCAAGATGAGCATTTCCCAATGAATATACAGTAACAT 517
 Db 61 ACATTTCAAGATGAGCATTTCCCAATGAATATACAGTAACAT 15
 RESULT 4
 A1248089/c 575 bp mRNA linear EST 01-DEC-1998
 LOCUS qh69f05.x1 Soares fetal_liver_spleen_INFLS.S1 Homo sapiens cDNA
 DEFINITION clone IMAGE:1849953.3' similar to gb:X57025_rnal INSULIN-LIKE
 GROWTH FACTOR IA PRECURSOR (HOMAN);, mRNA sequence.
 A1248089
 ACCESSION A1248089.1 GI:3843486
 VERSION EST.
 KEYWORDS human.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 575)
 REFERENCE NCI-CCRP http://www.ncbi.nlm.nih.gov/ncicrp.
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 TITLE Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bcrfemail.nih.gov
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 Insert Length: 918 Std Error: 0.00
 Seq primer: 40UP from Glibco
 High quality sequence stop: 380.
 Location/Qualifiers

source 1.575
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:194953"
 /clone_lib="Soares_fetal_liver_spleen_infls_si"
 /sex="male"
 /dev_stage="20 week-post conception fetus"
 /lab_host="DH10b (ampicillin resistant)"
 /note="Organ: Liver and Spleen; Vector: pT73 (Pharmacia) with a modified polylinker; Site_1: Pac I; Site_2: Eco RI; This is a subtracted version of the original Soares fetal liver spleen INFLS library. 1st strand cDNA was primed with a Pac I - Oligo(dT) primer [5', AACTGAGATTAATTAAGATCTTTTCTTTTCTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT 135 a 152 c 131 g 156 t 1 others
 ORIGIN

Query Match 63.2% Score 326.6; DB 9; Length 575;
 Best Local Similarity 86.6%; Pred.No.4.4e-86;
 Matches 438; Conservative 0; Mismatches 15; Indels 53; Gaps 5;

16 TCGGGGCTGAGCTGTGTGATGCTCTTCACTTGTGTGTGAGACAGGGGCTTTATTTC 75
 |||||
 551 TCGGGGCTGAGCTGTGTGATGCTCTTCACTTGTGTGTGAGACAGGGGCTTTATTTC 492
 |||||
 76 AACAGAGCCACAGGATGTGCTCCAGAGTCGAGAGGGGCGCTCAGACAGCATCGTGAT 135
 |||||
 491 AACAGAGCCACAGGATGTGCTCCAGAGTCGAGAGGGGCGCTCAGACAGCATCGTGAT 432
 |||||
 136 GAGTGTGCTTCCGAGAGCTGTATCTAAGAGGCTGAGATGTATTGCCGACCCCTCAAG 195
 |||||
 431 GAGTGTGCTTCCGAGAGCTGTATCTAAGAGGCTGAGATGTATTGCCGACCCCTCAAG 372
 |||||
 196 CCTCCAGAGTACGCTGCTCTGTCTGCGGAGCCAGCCACAGCATGCCAAGACCCAG 255
 |||||
 371 CCTCCAGAGTACGCTGCTCTGTCTGCGGAGCCAGCCACAGCATGCCAAGACCCAG 312
 |||||
 256 AAGTATGAGCCCATCTACCAACAGAACAGAACTCTAGAGAAAGAAAGAAATGACA 315
 |||||
 311 -----AAGAAAGTACA 301
 |||||
 316 TTTAAGACACAACTGTAGAGGAGTGCAGAAACAGAACTACAGATGA-CAAGACC 374
 |||||
 300 TTTAAGACACAACTGTAGAGGAGTGCAGAAACAGAACTACAGATGTAGAGAGACC 241
 |||||
 375 TTTCGAGAGTGAAGAGAGAGGAGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 433
 |||||
 240 TCCGAGAGTGAAGAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 181
 |||||
 434 -TAAACATTTGAATACGCGCCAAAAAATTAAGTTGATACATTTCAAGAT-GGCATTTC 491
 |||||
 180 TTAACCTTTGAAACACCTACCAAAAAAATTAAGTTGATTAACATTTAAAGATGGGCGTTTC 121
 |||||
 492 CCCCATGAATATACAAAGTAAACAT 517
 |||||
 120 CCCCAATGAATATACAAAGTAAACAT 95
 |||||

RESULT 5
 A1169253/c 549 bp mRNA linear EST 08-JAN-1999
 LOCUS EST215088 Normalized rat kidney, Bento Soares Rattus sp. cDNA clone
 DEFINITION RKBP33 3' end, mRNA sequence.
 ACCESSION A1169253
 VERSION A1169253.1 GI:4134375
 KEYWORDS EST.
 SOURCE Rattus sp.
 ORGANISM Rattus sp.

REFERENCE 1 (bases 1 to 549)
 AUTHORS Lee,N.H., Glodex,A., Chandra,I., Mason,T.M., Quackenbush,J., Kerlavage,A.R. and Adams,M.D.
 TITLE Rat Genome Project: Generation of a Rat EST (REEST) Catalog & Rat Gene Index
 JOURNAL Unpublished (1998)
 COMMENT On Oct 6, 1998 this sequence version replaced gi:3705561.
 OTHER_SEQS: TC50779
 CONTACT: Lee, NH
 The Institute for Genomic Research
 9712, Medical Center Drive, Rockville, MD 20850, USA
 Tel: (301)-838-3529
 Fax: (301)-838-0208
 Email: nhlee@tigr.org
 Seq primer: M13-21.

FEATURES
 source 1.549
 Location/Qualifiers
 /organism="Rattus sp."
 /db_xref="taxon:10118"
 /clone="RKBP33"
 /clone_lib="Normalized rat kidney, Bento Soares"
 /note="Organ: Kidney; Vector: pT73pac; Site_1: EcoRI; Site_2: NotI"

BASE COUNT 112 a 140 c 133 g 164 t
 ORIGIN

Query Match 61.2% Score 316.6; DB 9; Length 549;
 Best Local Similarity 80.8%; Pred.No.4e-83;
 Matches 421; Conservative 0; Mismatches 89; Indels 11; Gaps 4;

8 AGACGCTCGCGGGCTGAGCTGTGTGATGCTCTTCACTTGTGTGTGAGACAGGGGCT 67
 |||||
 549 AGACGCTTCCGGGCTGAGCTGTGTGAGCTCTTCACTTGTGTGTGAGACAGGGGCT 490
 |||||
 68 TTTATTTCACAAAGCCACAGGATGTGCTCCAGAGTCGAGAGGGGCGCTCAGACAGGCA 127
 |||||
 489 TTTACTTACAAAGCCACAGGATGTGCTCCAGAGTCGAGAGGGGCGCTCAGACAGGCA 430
 |||||
 128 TCGTGATGAGTGTGCTTCCGAGCTGTATCTAAGAGGCTGAGATGTATTGCCGAC 187
 |||||
 429 TGTGATGAGTGTGCTTCCGAGCTGTATCTAAGAGGCTGAGATGTATTGCCGCTC 370
 |||||
 188 CCTCAAGCTGCCAAGTACAGCTGCTGTCTGCGGAGCCAGCCAGCCAGCCAGCATGGCCA 247
 |||||
 369 CGCTGAAGCTTCAAAAGTACGCTGCTTCATCCGCGGCGCCAGCCAGCATGTGACATGCCA 310
 |||||
 248 AGACCCAGAGTATAGCCGCCCATCTACCAACAAAGACAGAACTCTCA---GAGAAGA 304
 |||||
 309 AGACTCAGAGTCCAGCCCATATGACACACAAGAAAGAGTGCAGAAAGAGGAAGA 250
 |||||
 305 AAGGAATTCATTTGAACACAAAGTGAAGGAGTGCAGAAACAAACTACAGAGTG 364
 |||||
 249 AAGGAAGTCACTTGAAGACAAAGTGAAGGAGTGCAGAAACAAACTACAGAGTG 190
 |||||
 365 TA-GAAGACCTTCTGAGAGTGAAGAGAGAGCCACCGGAGGAGGAGGAGGAGGAGGAG 423
 |||||
 189 TAGAGAGACCTCCCGAGAGACAGAAATGCCAGTCACCGGAATATCTTGTGCTGCTG 130
 |||||
 424 CAGTTACTGTAAACATTGGAATACCGGCA-----AAAAATTAAGTTGATACATTTTC 477
 |||||
 129 AGCAACCTGCAAAACATCGGAACACCTGCGCAATATCAATATGATTCATATACATTTTC 70
 |||||
 478 AAGAT-GGCATTTCCCAATGAATATACAGAGTAAACAT 517
 |||||
 69 AGAGATGGCATTTCCCTCAATGAATATACAGAGTAAACAT 29
 |||||

RESULT 6
 A1265629/c 558 bp mRNA linear EST 18-NOV-1998
 LOCUS A1265629

| DEFINITION | u04007.xl Suguano mouse liver mla Mus musculus cDNA clone |
|---|---|
| IMAGS:1890901.3' | similar to gb:X04482 Mouse mRNA for preproinsulin-like growth factor IB (MOUSE);, mRNA sequence. |
| ACCESSION | U1265629.1 GI:3883787 |
| VERSION | EST. |
| KEYWORDS | house mouse. |
| SOURCE | Mus musculus. |
| ORGANISM | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. |
| REFERENCE | 1 (bases 1 to 558) |
| AUTHORS | Maria,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Schellenberg,K., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R. |
| TITLE | The WashU-HMI Mouse EST Project |
| JOURNAL | Unpublished (1996) |
| COMMENT | Contact: Maria M/Mouse EST Project WashU-HMI Mouse EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@wustl.edu This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:975325 |
| FEATURES | Seq primer: custom primer used High quality sequence stop: 445. |
| SOURCE | Location/Qualifiers 1..558 /organism="Mus musculus" /strain="C57BL" /db_xref="taxon:10090" /clone="IMAGE:1890901" /clone_1ib="Suguano mouse liver mla" /sex="female" /dev_stage="adult" /lab_host="DH10B" /note="Organ: liver; Vector: pME185-FL3; Site:1: DraIII (CACCTGTGG); Site:2: DraII (CACCATGTGG). 1st strand cDNA was primed with an oligo(dT) primer [ATGGGCGCTTTTCTTTTCTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTGGCGCTTACTGG], digested and cloned into distinct DraIII sites of the pME185-FL3 vector (5' site CACCTGTGG, 3' site CACCATGTGG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Suguano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTCTGCTCTTAAAGCTGG and 3' end primer GCACCTGGAGCTGAGACA." |
| BASE COUNT | 106 a 135 c 156 g 161 t |
| ORIGIN | |
| Query Match | 61.1%; Score 315.8; DB 9; Length 558; |
| Best local Similarity | 80.8%; Pred No. 7e-83; |
| Matches 408; Conservative 0; Mismatches 87; Indels 10; Gaps 3 | |
| 0Y | 1 GGACCGGAGAGAGCGCTGCGGGGCTGAGCTGTGTGATGCTCTTCAGTTGCTGTGTGAGAGAC 60 |
| Db | |
| 506 | GGACCGAGAGACCCCTTGGCGGGCTGAGCTGTGTGATGCTCTTCAGTTGCTGTGTGAGAGAC 120 |
| 0Y | 61 AGGGCGCTTATTTCAACAAGCCACAGAGGTATAGTCTCCACAACTCGGAGGGCGCTCGAG 120 |
| Db | |
| 446 | AGGGCGCTTACTTCAACAAGCCACAGAGCTATGAGCTCCACAACTCGGAGGGCGACCTCAG 387 |
| 0Y | 121 ACAAGCATCGTGAGTGAAGTGTGCTTCCGAGAGCTGTGATCTAAGAGAGCTGGAATGTAT 180 |
| Db | |
| 386 | ACAAGCATGTGATGATGATGTGCTTCCGAGAGCTGTGATCTAAGAGAGCTGGAATGTAT 327 |
| 0Y | 181 TGGCACCCTCAAGCTGCCAAGTACAGTGCCTGTTCGCTGCCACAGCGCACACACGAC 240 |

| | | | | |
|---|---|-----|---|------------------------------------|
| D | b | | TGTCGCCCATCGAAGCTTACAAAAGCAGCCCGCTCTATCCGTGGCCAGCGGCACACTGAC | 267 |
| O | y | 241 | ATGCCCCAAGCCCAGAAGTATCAAGCCCCCATCTTACACAAAGAACAGAGTCTCA---G | 297 |
| D | b | 266 | ATGCCCCAAGACTCGAAGTCCCGCTCCCTATCGCAACAACAGAAMAAGAGCTTGCAAAGG | 207 |
| O | y | 298 | AGAAGGAAGAAGTAGTACATTGTGAAGAACACAGTAGAGGGGAGTGCAGAAACAAGAACTA | 357 |
| D | b | 206 | AGAAGGAAGAAGTAATCATTTTGGAGAACACAGTAGAGAGTAGTCAGAGAAACAAGACTTA | 147 |
| O | y | 358 | CAGAGTATA-GAAGACCCTTCTGAGAGAGTGAAGAAGACAGGCCAGCCAGACCCCTTG | 416 |
| D | b | 146 | CAGATATGTAGAGGAGCGCTCCACGAGAGCAGAAATATCCACATCACCGCAGAGTCTTTG | 87 |
| O | y | 417 | CTCTGCACAGTACTACCTGTAAACATTGSAAATACCGCCA-----AAAAATAGTTTATC | 470 |
| D | b | 86 | CTGCTTGAGCAACCTGCAAAACATCGAAGACCTCACAAATACAAATATATATAGTCACATA | 27 |
| O | y | 471 | ACATTTCAAAGATGGCATTTTCCCC 495 | |
| D | b | 26 | ACATTACAAAGATGGCATTTCCCC 2 | |
| R | E | S | RESULT 7 | |
| A | A | A | AA542914 | 498 bp mRNA linear EST 19-AUG-1997 |
| L | O | C | n198c10.s1 NCI-CGAP Pr21 Homo-sapiens cDNA clone IMAGE:984882.3' | |
| D | E | N | similar to db:X57025.nml INSULIN-LIKE GROWTH FACTOR IA PRECURSOR (HUMAN);, mRNA sequence. | |
| A | C | S | AA542914 | |
| V | E | R | AA542914.1 GI:2291394 | |
| K | E | Y | EST. | |
| S | O | U | human. | |
| O | R | G | Homo sapiens | |
| I | N | | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | |
| R | E | F | Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. | |
| J | I | T | 1 (bases 1 to 498) | |
| T | I | T | NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. | |
| J | O | R | National Cancer Institute, Cancer Genome Anatomy Project (CGAP), | |
| C | O | M | Tumor Gene Index | |
| J | O | R | Unpublished (1997) | |
| C | O | M | Contact: Robert Strausberg, Ph.D. | |
| J | O | R | Email: cgapso-remail.nih.gov | |
| C | O | M | Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R. | |
| J | O | R | Emmert-Buck, M.D., Ph.D. | |
| C | O | M | cDNA Library Preparation: M. Bento Soares, Ph.D. | |
| J | O | R | cDNA Library Arrayed by: Greg Lennon, Ph.D. | |
| C | O | M | DNA Sequencing by: Washington University Genome Sequencing Center | |
| J | O | R | clone distribution: NCI-CGAP clone distribution information can be | |
| C | O | M | found through the I.M.A.G.E. Consortium/LNL at: | |
| J | O | R | www.bio.linnl.gov/bdrip/image/image.html | |
| C | O | M | Insert Length: 603 Std Error: 0.00 | |
| J | O | R | Seq primer: -40m13 fwd. ET from Amersham | |
| C | O | M | High quality sequence stop: 412. | |
| J | O | R | Location/Qualifiers | |
| C | O | M | 1. .498 | |
| J | O | R | /organism="Homo sapiens" | |
| C | O | M | /db_xref="taxon:9606" | |
| J | O | R | /clone_image="984882" | |
| C | O | M | /clone_lib="NCI-CGAP-Pr21" | |
| J | O | R | /sex="male" | |
| C | O | M | /tissue_type="normal prostate" | |
| J | O | R | /lab_host="DHIOB" | |
| C | O | M | /note="Organ: prostate; Vector: pRT3D-Pac (Pharmacia) | |
| J | O | R | with a modified polylinker: 1st strand cDNA was prepared | |
| C | O | M | from normal prostate bulk tissue, and was then plined with | |
| J | O | R | a Not I - oligo(dT) primer. Double-stranded cDNA was | |
| C | O | M | ligated to Eco RI adaptors (Pharmacia), digested with Not | |
| J | O | R | I and cloned into the Not I and Eco RI sites of the | |
| C | O | M | modified pRT3 vector. Library is not normalized. Library | |
| J | O | R | was constructed by Bento Soares and M. Fatima Bonaldo." | |
| B | A | S | 105 a 135 c 123 g 135 t | |
| B | A | S | BASE COUNT | |

ORIGIN

Query Match 60.9%; Score 314.8; DB 9; Length 498;
 Best Local Similarity 86.2%; Pred. No. 1.3e-82;
 Matches 450; Conservative 0; Mismatches 17; Indels 55; Gaps 7;

QY 1 GGACCCGAGACGCTGCGGGGCGG-TGAGCTGGTGGATGCTCTTCAATTGCTGTGGAGA 59
 |||||
 DB 476 GGACCCGAGAACTTTGGGGGCTTGAAGTGGGAGTCTTCAATTGCTGTGGAGA 417
 60 CAGGGGCTTTATTTACACAGCCCAAGSGATGCTCCAGAGTCGAGGGGCGGCTCA 119
 |||||
 DB 416 CAGGGGCTTTATTTACACAGCCCAAGSGATGCTCCAGAGTCGAGGGGCGGCTCA 358
 120 GAAGAGCATGTGGATGAGTGGTCTTCCGGAGCTGTATCTAAGAGAGCTGGAATGTA 179
 357 GACAGGATGTGTGATGAGTGGTCTTCCGGAGCTGTATCTAAGAGAGCTGGAATGTA 298
 QY 180 TTGCGACACCCCTCAAGCTGCCAAGTCAGTCTGCTGCGCCAGCCGACACCGA 239
 |||||
 DB 297 TTGCGACACCCCTCAAGCTGCCAAGTCAGTCTGCTGCGCCAGCCGACACCGA 238
 240 CATGCCCAAGACCCAGAGTATCAGCCCCCATCTACACACAGACAGAGTCTAGAG 299
 |||||
 DB 237 CATGCCCAAGACCCAG----- 222
 300 AAGGAAAGAGATGATTTGAAGACACAGTAGAGGAGTGCAGGAAACAGACTACA 359
 |||||
 DB 221 -----AAGGAAAGATGATTTGAAGACACAGTAGAGGAGTGCAGGAAACAGACTACA 167
 360 GATGTA-GAAGACCTTCTGAGGAGTGAAGAGACAGGCCAGCCGAGACCTTTGCT 418
 |||||
 DB 166 GATGTAAGAGACCCCTGAGGAGTGAAGAGTGCAGTCCAGCCAGATCTTTGCT 107
 419 CTGAC-AGTACTCTG-TAAGATGGAATCCGGCAAAATAGTTGATCACTAT 476
 |||||
 DB 106 CTGACAGATTTACTCTGTTAACTTTGGAACACCTACCAAAAATTAAGTTGATCACTAT 47
 477 CAAGAT-GGCAATTTCCCAATGAATACACAGATAAAT 517
 |||||
 DB 46 AAAAGATGGCGTTTCCCAATGAATACACAGATAAAT 5

RESULT 8
 A119218 816 bp mRNA linear EST 02-SEP-1998
 LOCUS
 DEFINITION ue94h02.y1 Sugano mouse embryo mewa Mus musculus cDNA clone
 IMAGE:1498803 5' similar to gb:X0482 Mouse mRNA for
 preproinsulin-like growth factor IB (MUSE);, mRNA sequence.
 A119218
 ACCESSION A119218.1 GI:3519542
 VERSION
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 816)
 REFERENCE
 AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
 Gettel,S., Kucada,T., Lacy,M., Le,M., Martin,J., Morris,M.,
 Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
 Teisberg,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
 Waterston,R.
 TITLE The WashU-HMI Mouse EST Project
 JOURNAL Unpublished (1996)
 COMMENT Contact: Marra,M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.edu
 This clone is available royalty-free through LIND; contact the
 IMAGE Consortium (info@image.lind.gov) for further information.

MG1:936407
 Seq primer: custom primer used
 High quality sequence stop: 473.
 Location/Qualifiers
 1. 816
 /organism="Mus musculus"
 /strain="C57BL"
 /db_xref="taxon:10090"
 /clone="IMAGE:1498803"
 /clone_1db="Sugano mouse embryo mewa"
 /dev_stage="embryo, 14 dpc"
 /lab_host="DH10B"
 /note="Vector: pME18-FL3; Site 1: DraII (CACTGTG);
 Site 2: DraII (CAGCATGTG); 1st strand cDNA was primed
 with an oligo(dT) primer (ATGGGCGCTTTTCTTTTCTTTT);
 double-stranded cDNA was ligated to a DraII adaptor
 (TGTGGCTCTGTGG), digested and cloned into distinct DraII
 sites of the pME18-FL3 vector (5' site CACTGTG, 3' site
 CAGCATGTG). XhoI should be used to isolate the cDNA
 insert. Size selection was performed to exclude fragments
 <1.5kb. Library constructed by Dr. Sumio Sugano
 (University of Tokyo Institute of Medical Science).
 Custom primers for sequencing: 5' end primer
 CTTCGCTTAAGACTGCG and 3' end primer
 CGACTCGAGCTCGAGCA."

BASE COUNT 230 a 219 c 172 g 187 t 8 others

ORIGIN

Query Match 59.8%; Score 309; DB 9; Length 816;
 Best Local Similarity 80.2%; Pred. No. 8.2e-81;
 Matches 384; Conservative 0; Mismatches 91; Indels 4; Gaps 2;

QY 1 GGACCGAGACGCTGCGGGGCTGAGCTGTGATGCTCTTCAATTGCTGTGGAGC 60
 |||||
 DB 323 GGACCGAGACGCTTTCGGGGCTGAGCTGTGATGCTCTTCAATTGCTGTGGAGC 382
 61 AGGGCTTTTATTTAAAGAGCCACAGGATGCTCCACAGTCCGAGGCGGCTTCAG 120
 |||||
 DB 383 AGGGCTTTTATTTAAAGAGCCACAGGATGCTCCACAGTCCGAGGCGGCTTCAG 442
 121 ACAGCATGTGATGATGATGCTGCTTCGAGAGCTGTGATCAGAGAGCTGGAGATGAT 180
 |||||
 DB 443 ACAGCATGTGATGATGATGCTGCTTCGAGAGCTGTGATCAGAGAGCTGGAGATGAT 502
 181 TGGCAGCCCTTAAGCTGCGCAAGTACGTGCTGTGCTGCCAGCGCCACACCGAC 240
 |||||
 DB 503 TGGCAGCCCTTAAGCTGCGCAAGTACGTGCTGTGCTGCCAGCGCCACACCGAC 562
 241 ATGCCCAAGACCCAGAGATGAGCCCAATCTACCAAGAGACAGACAGTCTCA--G 297
 |||||
 DB 563 ATGCCCAAGACCCAGAGATGAGCCCAATCTACCAAGAGACAGACAGTCTCA--G 622
 298 AGAAGAAAGAGATGATTTGAAGACACAGTAGAGGAGTGCAGAGAAACAGACTA 357
 |||||
 DB 623 AGAAGAAAGAGATGATTTGAAGACACAGTAGAGGAGTGCAGAGAAACAGACTA 682
 358 CAGGATGTA-GAAGACCTTCTGAGAGTGAAGAGAGAGAGCCAGGAGGAGGAGCTTTG 416
 |||||
 DB 683 CAGGATGTAAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 742
 417 CTCTGACACGTTACTGTAACTTGAATACCGGCCAAATAATAGTTGATCACTAT 475
 |||||
 DB 743 CTCTGACACGTTACTGTAACTTGAATACCGGCCAAATAATAGTTGATCACTAT 801

RESULT 9
 BF383724 594 bp mRNA linear EST 27-NOV-2000
 LOCUS
 DEFINITION 602044632F1 NCI-CGAP_L19 Mus musculus cDNA clone IMAGE:4194295 5',
 mRNA sequence.
 ACCESSION BF383724
 VERSION BF383724.1 GI:11365029
 KEYWORDS EST.

SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Mammalia; Euthera; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 594)
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapds-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LMNL at: <http://image.llnl.gov>
Plate: LLM9527 row: p column: 08
High quality sequence stop: 589.
Location/Qualifiers
1..594
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone_image="4194295"
/clone_lib="NCI-CGAP_L19"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: liver; Vector: pCMV-Sport6; Site: 1; NotI; Site: 2; SalI; Cloned unidirectionally; Primer: oligo dt. Average insert size 1.9 kb. Constructed by Life Technologies. Note: this is a NCI-CGAP library."
BASE COUNT 175 a 162 c 142 g 115 t
ORIGIN
Query Match 58.7%; Score 303.6; DB 12; Length 594;
Best Local Similarity 80.7%; Pred. No. 3e-79; Mismatches 394; Conservative 0; Indels 10; Gaps 3;
Matches 394; Conservative 0; Mismatches 394; Conservative 0; Indels 10; Gaps 3;
16 TCGGGGGCTGAGCTGGTGGATGCTTTCAGTTCGTGTGGAGACAGGGGCTTTATTTTC 75
107 TCGGGGGCTGAGCTGGTGGATGCTTTCAGTTCGTGTGGAGACAGGGGCTTTATTTTC 166
76 AACAGCCACAGGGTATGGCTCCAGCAGCTGGAGGGGCTCCAGAGGAGCATCTGGAT 135
167 AACAGCCACAGGGTATGGCTCCAGCAGCTGGAGGGGCTCCAGAGGAGCATCTGGAT 226
136 GAGTCTGCTTCGGAGCTGTGATCTAAGAGGCTGGAGATGTATTGCCACCCCTCAAG 195
227 GAGTCTGCTTCGGAGCTGTGATCTAAGAGGCTGGAGATGTATTGCCACCCCTCAAG 286
196 CCTGCCAGTCAAGCTCGCTCTGTCCGTGCCAGCCGACACCGACATGCCCAAGACCAG 255
287 CCTACAAAAGCAGCGCTCTATCCGTCCGCGCCAGCCACATGCAATGCCCAAGCTAG 346
256 AAGTATCAGCCGCCCTCTACCAACAAGACAGAGTCTCA---GAGAAGAAAGAGT 312
347 AAGTCCCGCTCCCTATCGACAACAAGAAAGAGAGCTGCAAAAGAGAGAGAGT 406
313 AATTTTGAAGACACAGTGAAGAGTGAAGAGAGAGAGAGAGAGTGA---GAAGA 371
407 AATTTTGAAGACACAGTGAAGAGTGAAGAGAGAGAGAGAGAGTGA---GAAGA 466
372 CCCTTCGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTGA 431
467 GCCTCCAGT 526
432 TGTAAACATTTGATACGGGCA-----AAAAATAGTTGATACATTTCAAGATGG 485
527 GCAAAACATCGAAGACACCTACCAATTAACAATTAAGTCAATTAACATTAAGATGG 586
486 CATTTGCC 493
587 GCATTGCC 594

RESULT 10
AA913900/c
LOCUS
DEFINITION
AA913900 527 bp. mRNA linear EST 24-SEP-1998
c13505.s2 Soares_NFL_T.GBC_S1 Homo sapiens CDNA clone
IMAGE:1525496.3 similar to gb:X57025.rna1 INSULIN-LIKE GROWTH
FACTOR 1A PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION
AA913900
VERSION
AA913900.1 GI:3053292
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 527)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
JOURNAL
Contact: Robert Strausberg, Ph.D.
Email: cgapds-remail.nih.gov
This clone is available royalty-free through LMNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 870 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 97.
Location/Qualifiers
1..527
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="1525496"
/clone_lib="Soares_NFL_T.GBC_S1"
/lab_host="DH10B"
/note="Organ: pooled; Vector: pRTT3D-Pac (Pharmacia) with
a modified polylinker; Site: 1; Not I; Site: 2; Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NbHL19w, testis NRT, and B-cell
NCI-CGAP_GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo."
BASE COUNT 125 a 134 c 119 g 149 t
ORIGIN
Query Match 58.0%; Score 299.8; DB 9; Length 527;
Best Local Similarity 85.5%; Pred. No. 3.9e-78; Mismatches 413; Conservative 0; Indels 17; Gaps 5;
Matches 413; Conservative 0; Mismatches 413; Conservative 0; Indels 17; Gaps 5;
39 TCTTCAAGTTCGTGTGGAGACAGGGGCTTTATTTTCAACAGCCACAGGATATGCTC 98
527 TCTTCAAGTTCGTGTGGAGACAGGGGCTTTATTTTCAACAGCCACAGGATATGCTC 468
99 CAGAGTCGAGAGGGGGCTTACAGAGCATCTGATGATGCTTCGGAGCTGTGA 158
467 CAGAGTCGAGAGGGGGCTTACAGAGCATCTGATGATGCTTCGGAGCTGTGA 408
159 TCTAAGAGAGTGAAGATGTATTTCGACACCCCTCAAGCTGCAAGTCAAGTGGCTGTG 218
407 TCTAAGAGAGTGAAGATGTATTTCGACACCCCTCAAGCTGCAAGTCAAGTGGCTGTG 348
219 CCGTGGCCAGGCGCCACACGACATGCCCCAAGAGTCAAGTCAAGTGGCTGTG 278
347 CCGTGGCCAGGCGCCACACGACATGCCCCAAGAGTCAAGTCAAGTGGCTGTG 311
279 CAGAGACGAGAGTCTCAGAGAGAGAGAGATTTGAAGACACAGTGAAGAGGA 338
310 -----AAGGAGTACATTGTAAGAGAGAGAGAGAGGA 277

OY 339 GTGCGAGAAACAGAACTACAGATGTA-GAAGACCCCTTCTGAGAGTAAAGAGACAG 397
 DB 276 GTGCGAGAAACAGAACTACAGATGTAAGAGACCCCTCTGAGAGTAAAGAGATGACAT 217
 OY 398 GCCACCCGAGACCCCTTCTGCTGCGAC-AGTTACCGT-TAAACATGGAATACCGGCCAA 455
 DB 216 GCCACCCGAGATCCCTTCTGCTGCGACAGACTTACCTGTTAACTTTGGAACACTACCA 157
 OY 456 AAATAAGTTGATCATTTCACAAAGAT-GGCATTTCGCCCAATGAATACACACTAA 514
 DB 156 AAATAAGTTGATTAACATTAAAGATGGCGCTTCCCAATGAATACACACTAA 97
 OY 515 CAT 517
 DB 96 CAT 94
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 A1876493/c
 LOCUS
 DEFINITION A1876493 642 bp mRNA linear EST 21-JUL-1999
 U359b10.x1 Sugano mouse liver m1a Mus musculus cDNA clone
 IMAGE:1924219.3 similar to gb:X57025.fna1 INSULIN-LIKE GROWTH
 FACTOR IA PRECURSOR (HUMAN); gb:X04482 mouse mRNA for
 preproinsulin-like growth factor IB (MOUSE); mRNA sequence.
 A1876493
 VERSION
 KEYWORDS
 SOURCE EST.
 ORGANISM
 house mouse.
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 642)
 Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
 Underwood, K., Streps, M., Theising, B., Allen, M., Bowers, Y., Person,
 B., Swaller, T., Gibbons, M., Page, D., Harvey, N., Schurk, R., Ritter,
 E., Kohn, S., Shin, T., Jackson, I., Cardenas, M., McCann, R.,
 Waterston, R., and Wilson, R.
 The WashU-NCI Mouse EST Project 1999
 Unpublished (1999)
 Contact: Marra M/WashU-NCI Mouse EST Project 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.edu
 This clone is available royalty-free through LIND; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:990511
 Seq primer: custom primer used
 High quality sequence stop: 257.
 Location/Qualifiers
 1. 642
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 /strain="C57BL"
 /db_xref="taxon:10090"
 /clone="IMAGE:1924219"
 /clone_1kb="Sugano mouse liver m1a"
 /sex="Female"
 /dev_stage="adult"
 /lab_host="DH10B"
 /note="Organ: liver; Vector: pME18S-FL3; Site: 1: DraIII
 (CACATGTC); Site: 2: DraIII (CACCATGTG); 1st strand cDNA
 was primed with an oligo(dT) primer
 [ATGTGGCCTTTTCTTTTCTTTT]; double-stranded cDNA was
 ligated to a DraIII adaptor [TGTGGCCTTCTG]; digested
 and cloned into distinct DraIII sites of the pME18S-FL3
 vector (5' site CACATGTC, 3' site CACCATGTG). XhoI should
 be used to isolate the cDNA insert. Size selection was
 performed to exclude fragments <1.5kb. Library
 constructed by Dr. Sumio Sugano (University of Tokyo
 Institute of Medical Science). Custom primers for
 sequencing: 5' end primer CTCTGCTCTTAAAGCTGCG and 3' end
 primer CGACCTGCAAGCTGACACA."

BASE COUNT 127 a 154 c 175 g 185 t 1 others
 ORIGIN
 Query Match
 Best Local Similarity 78.9%; Score 289.6; DB 9; Length 642;
 Matches 397; Conservative 0; Mismatches 95; Indels 11; Gaps 4;
 OY 2 GACCGGAGAGCTCTGGGGGCTGAGCTGTGATGCTCTTCACTGCTGTGAGACA 61
 DB 503 GACCGAGAGACCCCTTTCGGGGCTGAGCTGTGATGCTCTTCACTGCTGTGAGACA 444
 OY 62 GGGCTTTTATTTCAACAAGGCTATNGGCTCCAGAGTGGAGGGGCGCTCAGA 121
 DB 443 GGGGCTTTTCTTCAACAAGGCTATNGGCTCCAGAGTGGAGGGGCGCTCAGA 384
 OY 122 CAGCATGCTGATGATGCTGCTCTCCG-AGCTGTATCTAAGAGGCTGAGATGTAT 180
 DB 383 CAGTCATATGTGATGATGCTGCTCTCCGAGAGCTGTATCTGAGAGAGCTGATGATG 324
 OY 181 TCGGACCCCTTCAACCTTCCAGAGTACCTGCTGTCTGCTGCCACGACACACAC 240
 DB 323 TGTGCCCCCACTGAACCTTCAAAAGACCCGCTCTATCCGTGCCACGACACCTGAC 264
 OY 241 ATGCCCAAGACCCAGAGATATCAGCCCATCTACCAACAAGACACGAGTCTCA--G 297
 DB 263 ATGCCCAAGACTCAAGAGTATCCCGCTCTATGACAAACAAAGAACGAGCTGAAAG 204
 OY 298 AGAAGGAAGAGATGATCTTTGAGAGACAGATGAGAGGCTGACGAGAAACAGACTA 357
 DB 203 AGAAGGAAGAGATGATCTTTGAGAGACAGATGAGAGGCTGACGAGAAACAGACTA 144
 OY 358 CAGCATGTA-GAAGACCCCTTCTGAGAGTGAAGAGACAGAGCCACCCAGACCTTTG 416
 DB 143 CAGATGTAGAGAGAGCTCCACGAGACAGAAATGCCATATCACCAGATCTTTG 84
 OY 417 CTCTGCAAGTACTCTGTAACATTTGAAATACCGGCA-----AAAATAGTTGATC 470
 DB 83 CTGCTTGAGCAACCTCGCAAAACATCGAAACACTACCAATATATAGTCAATA 24
 OY 471 ACATTCAAGATGATCTTCC 493
 DB 23 ACATTCAAGATGATCTTCC 1
 RESULT 12
 AM495481/c
 LOCUS
 DEFINITION AM495481 499 bp mRNA linear EST 24-FEB-2000
 UI-M-BH3-ay-9-11-0-UI.s1 NIH.BMAP.M.S4 Mus musculus cDNA clone
 AM495481
 VERSION
 KEYWORDS
 SOURCE EST.
 ORGANISM
 house mouse.
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 499)
 Bonaldo, K.F., Lennon, G. and Soares, M.B.
 Normalization and subtraction: two approaches to facilitate gene
 discovery
 Genome Res. 6 (9), 791-806 (1996)
 97044477
 JOURNAL
 MEDLINE
 COMMENT
 Contact: Chn. H
 National Institute of Mental Health
 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
 20892-9643, USA
 Tel: 301 443 1706
 Fax: 301 443 9890
 Email: mestr@mail.nih.gov
 The sequence contained an oligo-dT track that was present in the
 oligonucleotide that was used to prime the synthesis of first A
 strand cDNA and therefore this may represent a bonafide poly A
 tail. The sequence tag present in the cDNA between the NotI site

QY 300 AAGGAAGAAGTAATTGATTTGGAAGAACACAAATTAAGGAGATGCAAGGAAACAAATCTAAC 359

Db 228 AAGGAAGAAGTAATTGATTTGGAAGAACACAAATTAAGGAGATGCAAGGAAACAAATCTAAC 169

QY 360 GGATGTA-GAAGACCCCTTCTGAGAGTGAAGAGGACAGCCACCCGACGCCCTTTGCT 418

Db 168 GAATGTAGAAGAGAGCTCCCGAGAACAGAAATATGCCAGCTACACCGCAAGATCCTTTGCT 109

QY 419 CTGCACAGTTACTCTGTAAACATTGAATACCGGCCA-----TAAATTAAGTTGATCAC 472

Db 108 GCTTGAGCAACCTGGCAAAACATCGGAACACCTGGCAAAATACATATATGATGTTCAATACC 49

QY 473 ATTTCAAAGAT-GGCATTTTCCCCCATCAATATACACAGTAAACAT 517

Db 48 ATTTCAGAGATGGCATTTCCCTCAATTAATATACCAAGTAAACAT 3

| | |
|------------|---|
| RESULT | 14 |
| A1604642 | |
| LOCUS | |
| DEFINITION | A1604642 882 bp mRNA linear EST 21-APR-1997 |
| | yM43308.y1 Stratagene mouse diaphragm (#937303) Mus musculus cDNA |
| | clone IMAGE:100107 5' similar to gb:M11568 INSULIN-LIKE GROWTH |
| | FACTOR IB PRECURSOR (HUMAN); gb:X04482 Mouse mRNA for |
| | proinsulin-like growth factor IB (MOUSE); , mRNA sequence. |
| ACCESSION | A1604642 |
| VERSION | A1604642.1 GI:4613809 |
| KEYWORDS | EST. |
| SOURCE | house mouse, |
| ORGANISM | Mus musculus |

| REFERENCE | AUTHORS | TITLE | JOURNAL | COMMENT |
|--|--|--------------------------------------|---------|---------|
| (Pages 1 to 882) | | | | |
| Marrar,M., Hiller,L., Kucaba,T., Martin,J., Beck,C.C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurr,R., E., Konn,S., Shin,T., Jackson,Y., Cardenas,K., Mcconn,R., Mateston,R., and Wilson,R. | | The Mashu-NCI Mouse EST Project 1999 | | |
| | | Unpublished (1999) | | |
| Contact: | Maria M/Mashu-NCI Mouse EST Project 1999 | | | |

TITLE The Mashu-NCI Mouse EST Project 1999
 JOURNAL Unpublished (1999)
 COMMENT Contact: Maria W/Mashu-NCI Mouse EST Project 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LNL / contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 MGI:665223
 This read is a RESEQUENCE of a previously sequenced mouse clone
 This read has been verified (found to hit its original self in the
 correct orientation)
 Seq primer: -40RP from Gibco
 High quality sequence s-top:361.

| FEATURES | Location/Qualifiers |
|----------|---------------------|
| source | 1. .882 |

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/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:1001007"
/clone_lib="Stratagene mouse diaphragm (#937303)"
/tissue_type="diaphragm"
/dev_stage="adult"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: diaphragm; Vector: Bluescript SK-; Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally from mRNA prepared from diaphragm muscle. Primer: Oligo dT. Averag insert size: 1.5 kb. Uni-ZAP XR vector; ~5' adaptor sequence: 5' GAATTCGACACGAG 3' ~3' adaptor sequence: 5' CTCGACATTTTCTTTTCTTTT 3'"

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| Query Match | Score | DB | Length |
|-----------------------|--------|--------------------|--------|
| Best Local Similarity | 53.1%; | 9; | 882; |
| | 75.6%; | Pred. No. 1.6e-70; | |

Matches 384; Conservative 0; Mismatches 115; Indels 9; Gaps 4;

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| QY | 1 | IGAGCGGAACACGCTTGGCGGGCTAGCGTGGATGATCTTTAGTTCGCTGTGGAGAC | 60 |
| Db | 377 | GGACCGAAGACCCCTTGGCGNGCTGAGGTGATGGATGCTCTTCAGTTTCGTGTGGACCG | 436 |
| QY | 61 | AGGGGCTTTATTTACACAGGCCACAGAGTATGCTGTCAGCAGTGGAGGGCGCTCAG | 120 |
| Db | 437 | AGGGGCTTTACTTACACAGGCCACAGAGCTATGCTGCCAGCATTTTCAGGGCAGCTCAG | 496 |
| QY | 121 | ACAGGCATGCTGATGAGAGTGGCTGCTCCGAGAGCTGATATTAAGAGAGCTGGAGATGTAT | 180 |
| Db | 497 | ACAGGATTTGTGATGATGATGTTGCTTCGGAGAGCTGTATCTGANGAGACTGGAGATGTAC | 556 |
| QY | 181 | TGCGCACCCCTCAAGCCTGGCAAGTCAGCTCGCTGTGCTCGTGCCAGCGCCACACCGAC | 240 |
| Db | 557 | TGTGCCCCCTCAAGACCTACANAAAGCACCCGCTCTCTCCGTCGCCAGCGCCACACATGAC | 616 |
| QY | 241 | ATGCCCAACAGCCAGAGATACAGCCCCCATCTCCACAAGAGACAGAGTCTCAGAG | 299 |
| Db | 617 | ATGCCNAGACCTCAAGAGTCCCGCTGCTATTCGACNNAAAGAGAAAGAGAGCTTGCAGAG | 676 |
| QY | 300 | -AAGGAAGAAGATACATTTGAAGAACACAGTAGAGGGAGTGCAGAGAAACAAGACTA | 357 |
| Db | 677 | GAGAGGGAAGGAGATACATTTGAGGAACACANGTNGAGGAAGTGCANGAAGAACACTTA | 736 |
| QY | 358 | CAGAGCTGAGAGACCCCTTCTGAGAGATGAGAGAGAGACGAGCCACCGCAGAGACCTTGC | 417 |
| Db | 737 | CCAGATGATNMGAGAGCCCT-TCAACCGAGCGAAGATGCACATCCCGNAGATCTTTTGC | 795 |
| QY | 418 | TCTGCACAGATTACCTGTTAAACATTTGGAAATACCGGACAA- -AAATTAAGTTGATCACA | 473 |
| Db | 796 | T-GCTTAGACCTAAGTCGAACATGCAACCACTTACCAATTACATATAATAGTTCAATTAAC | 854 |
| QY | 474 | TTTCAAGATGCGCATTTCCCGCAATGAA | 501 |
| Db | 855 | ATTCAGAGATGGCATTTCCCGCATTTGAA | 862 |

| | |
|------------|--|
| RESULT 15 | |
| AI478804/c | |
| LOCUS | 430 bp mRNA linear EST 14-APR-199 |
| DEFINITION | tm52804.x1 NC1 CGAP Kid1 Homo sapiens cDNA clone IMAGE:2161758 3' similar to gb.X57025.ra1 INSULIN-LIKE GROWTH FACTOR 1A PRECURSOR (HUMAN); mRNA sequence. |
| ACCESSION | AI478804 |
| VERSION | AI478804.1 |
| KEYWORDS | GT:4373617 |
| SOURCE | EST. |
| ORGANISM | human. |
| | Homo sapiens |

| | |
|-----------|--|
| REFERENCE | Mammalian, Eukaryotic, Prokaryotic, Archaeal, Plant, Animal, Human, Mouse, Rat, Fish, Invertebrate, Microbe. |
| AUTHORS | I (bases 1 to 430) |
| TITLE | NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap . |
| JOURNAL | National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index |
| COMMENT | Unpublished (1997) Contact: Robert Strausberg, Ph.D. |

Email: cgabbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCAP clone distribution information can be found through the I.M.A.G.E. Consortium/ILM at: www.bio.ln1.gov/bnrf/image/image.html
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Seq primer: -400P from Gibco
High quality sequence stop: 411.

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FEATURES      Location/Qualifiers
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              /organism="Homo sapiens"

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/clone_image="2161758"
/clone_lib="NCI_CGAP_Kid11"
/lab_host="DH10B"
/note="Organ: Kidney; Vector: PT73D-Pac (Pharmacia) with
a modified polylinker: Site 1: Not I; Site 2: Eco RI;
Plasmid DNA from the normalized library NCI_CGAP_Kid1 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneids 132376-132391, 145607-145675, and
150052-150285). Subtraction by Bento Soares and M.
Fatima Bonaldo."

```

BASE COUNT 96 a 93 c 103 g 138 t

ORIGIN

Query Match 51.9%; Score 268.2; DB 9; Length 430;
 Best Local Similarity 95.0%; Pred. No. 9.2e-69;
 Matches 320; Conservative 0; Mismatches 13; Indels 4; Gaps 4;

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Db 430 CACCCCTAAGCCTGCCAAGTCAGCTCGCTCTGTCGCGCCAGCCGACACCGCATGC 371
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QY 245 CCAAGACCCAGAGATATCAGCCCCCATCTACCAACAGAGACGAGTCTCAGAGAAAGA 304
    |||||||
Db 370 CCAAGACCCAGAGATATCAGCCCCCATCTACCAACAGAGACGAGTCTCAGAGAAAGA 311
    |||||||
QY 305 AAGGAGTACATTTGAGAGACACAAGTAGAGGAGTGCAGAGAAACAAGACTACAGGATG 364
    |||||||
Db 310 AAGGAGTACATTTGAGAGACACAAGTAGAGGAGTGCAGAGAAACAAGACTACAGGATG 251
    |||||||
QY 365 TA-GAAGACCTTCTGAGAGAGTGAAGAGACAGGCCAGGACGACCTTGTCTGCA 423
    |||||||
Db 250 TAGGAAGACCTTCTGAGAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAG 191
    |||||||
QY 424 C-AGTTACCTG-TAAACATGGAATACCGGCCCAAAATAAATTGATGACATTTCAAAG 481
    |||||||
Db 190 CGAGTTACCTGTTAACTTTGGAACACCTACCAAAAATAAATTGATGATTAACATTTAAAG 131
    |||||||
QY 482 AT-GGCATTTCGCCCAATGAATACCAAGTAAACAT 517
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Db 130 ATGGCGTTTCCCAATGAATACCAAGTAAACAT 94
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Search completed: June 15, 2003, 18:18:21
 Job time : 1104.81 secs